

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2006, 05:21:02 ; Search time 5453 Seconds  
(without alignments)  
11058.577 Million cell updates/sec

Title: US-09-857-346A-2

Perfect score: 943

Sequence: 1 cgagaaagagaaaaaa.....tgagaaaaaa..... 943

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_env.\*  
2: gb\_pat.\*  
3: gb\_ph.\*  
4: gb\_pl.\*  
5: gb\_pr.\*  
6: gb\_to.\*  
7: gb\_sts.\*  
8: gb\_sy.\*  
9: gb\_un.\*  
10: gb\_vi.\*  
11: gb\_ov.\*  
12: gb\_htg.\*  
13: gb\_in.\*  
14: gb\_om.\*  
15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	943	100.0	943	2	BD272883
2	943	100.0	943	4	AF116527
3	792	84.0	806	4	AY964095
4	787.2	83.5	806	4	AY964094
5	784.4	83.2	797	2	BD268759
6	784.4	83.2	797	2	AR476092
7	784.4	83.2	801	4	AF537203
8	770.8	81.7	774	4	AY850001
9	686	72.7	842	4	AY850000
10	680	72.1	732	4	AY850002
11	593.8	63.0	651	4	DQ167446
12	591	62.7	591	4	AY964092
13	591	62.7	599	4	AY964097
14	591	62.7	599	4	AY964093
15	587.4	62.3	651	4	DQ167444
16	587	62.2	591	4	AY964090
17	543	57.6	591	4	DQ167447
18	538.4	57.1	868	2	BD272888

19	528	56.0	845	2	BD272892	BD272892	Control o
20	528	56.0	845	4	AY036888	AY036888	Brassica
21	527	55.9	891	2	BD272894	BD272894	Control o
22	523.4	55.5	565	4	AY964091	AY964091	Arabidops
23	494.8	52.5	969	2	BD272887	BD272887	Control o
24	494.8	52.5	969	4	AY036890	AY036890	Brassica
25	491.8	52.2	851	4	AY364013	AY364013	Brassica
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27	488.4	51.8	666	4	AY306123	AY306123	Brassica
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29	480.4	50.9	822	4	AY308848	AY308848	Brassica
30	477.4	50.6	908	2	BD272885	BD272885	Control o
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32	471.4	50.0	780	2	BD272891	BD272891	Control o
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42	451.6	47.9	594	4	AY273165	AY273165	Brassica
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#### ALIGNMENTS

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ACCESSION	BD272883.1	GI:33082651			
VERSION	JP 2002532069-A/2.				
KEYWORDS	Arabidopsis thaliana (thale cress)				
SOURCE	Arabidopsis thaliana				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.				
REFERENCE	1 (bases 1 to 943)				
AUTHORS	Burn,J.E., Peacock,W.J., Dennis,E.S., Sheldon,C.C., Perez,P., Helliwell,C.A. and Rouse,D.T.				
TITLE	Control of flowering				
JOURNAL	Patent: JP 2002532069-A 2 02-OCT-2002;				
COMMENT	COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION, PASCUAL PEREZ				
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	PN JP 2002532069-A/2				
	PD 02-OCT-2002				
	PP 02-DEC-1999	JP 2000585411			
	PR 03-DEC-1998	AU PP 7469,22-JAN-1999	US	60/116928	PI
	JOANNE ELIZABETH BURN, WILLIAM JAMES PEACOCK, ELIZABETH PI				
	SALISBURY DENNIS,				
	PI CANDICE CLAIRE SHELTON, PASCUAL PEREZ, CHRISTOPHER ANDREW PI				
	HELLIWELL,				
	PI DEAN THOMAS ROUSE				
	PC C12N15/09,A01H5/00,C07K14/415,C07K16/16,C12N5/10,C12Q1/68, PC				
	G01N33/48,				
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	of flowering				
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source					

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Qy	361	GTCAAAAGCTCTGAATGTGTAAGTGTGAGTCTTGTGTAAGCTTGTGATGATCA	420
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Db	781	CGCTGATTAAGGGCGAGCGTTGTATATCTTAAATCTCTCTTTTGGGCAAGACTTTG	840
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Db	841	TGTGTGATCTTAAGTACGAGAACTAAGTCAATCTCTGTTTAAAGCAAAAGTTG	900
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RESULT 2

AF116527

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

AUTHORS

TITLE

JOURNAL

PUBMED

FEATURES

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ORIGIN

Query Match

Best Local Similarity

Matches 943;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Qy

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Db

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Db 361 GTCAAAAGCTCTGAACCTATGGTTTCACACTATGAGCTACTTGAACCTTGGATAGCAAGCT 420  
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RESULT 3  
LOCUS AY964095 806 bp mRNA linear PLN 03-AUG-2005  
DEFINITION Arabidopsis thaliana isolate N1337 flowering locus C protein mRNA, complete cds.  
ACCESSION AY964095  
KEYWORDS AY964095.1 GI:62632902  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
1 (bases 1 to 806)  
Lempe,J., Balasubramanian,S., Sureshkumar,S., Singh,A., Schmid,M. and Weigel,D.  
Diversity of Flowering Responses in Wild Arabidopsis thaliana Strains  
Plos Genet. 1 (1), E6 (2005)  
16103920  
2 (bases 1 to 806)  
Lempe,J., Balasubramanian,S., Sureshkumar,S., Singh,A., Schmid,M. and Weigel,D.  
Direct Submission  
Submitted (16-MAR-2005) Department of Molecular Biology, Max Planck Institute for Developmental Biology, Spemannstrasse 37-39, 72076 Tuebingen, Germany  
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DEFINITION	AY964094			
ACCESSION	AY964094.1 GI:62632900			
VERSION				
KEYWORDS	Arabidopsis thaliana (thale cress)			
SOURCE	Arabidopsis thaliana			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi			
REFERENCE	1 (bases 1 to 806)			
AUTHORS	Lempe,J., Balasubramanian,S., Sureshkumar,S., Singh,A., Schmid,M. and Weigelt,D.			
TITLE	Diversity of Flowering Responses in Wild Arabidopsis thaliana Strains			
JOURNAL	PLoS Genet. 1 (1), E6 (2005)			
PUBMED	16103920			
REFERENCE	2 (bases 1 to 806)			
AUTHORS	Lempe,J., Balasubramanian,S., Sureshkumar,S., Singh,A., Schmid,M. and Weigelt,D.			
TITLE	Direct Submission			
JOURNAL	Submitted (16-MAR-2005) Department of Molecular Biology, Max Planck Institute for Developmental Biology, Spemannstrasse 37-39, 72076 Tuebingen, Germany			
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QY	318 A T C G G A A C A G C A T C G T G A T G A T C T T A A G C C T T G G A T C A T C A G T C A A A G C T C T G A C T 377			
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Query Match		83.2%;	Score 784.4;	DB 2;	Length 797;
Best Local Similarity		99.9%;	Pred. No. 2.2e-233;		
Matches 785;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
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Qy	230	GCATCCGTCGCTCTTCTCGTCTCTCCGCTCCGCGCAAGCTCTACAGCTTCTCTCCCGGC	289		
Db	121	GCATCCGTCGCTCTTCTCGTCTCTCCGCTCCGCGCAAGCTCTACAGCTTCTCTCCCGGC	180		
Qy	290	GATACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTTAAAGCC	349		
Db	181	GATACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTTAAAGCC	240		
Qy	350	TTGGATCATCATGTCAAAAGCTCTGAACTATGGTTTCACTATGAGCTACTTGAACCTTGTG	409		
Db	241	TTGGATCATCATGTCAAAAGCTCTGAACTATGGTTTCACTATGAGCTACTTGAACCTTGTG	300		
Qy	410	GATAGCAAGCTTTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCACCTG	469		
Db	301	GATAGCAAGCTTTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCACCTG	360		
Qy	470	GAGGAACACCTTGAGACTGCCCTCTCCGTGACTAGAGCCAAAGAACCGAACTCATGTTG	529		
Db	361	GAGGAACACCTTGAGACTGCCCTCTCCGTGACTAGAGCCAAAGAACCGAACTCATGTTG	420		
Qy	530	AAGCTTGTGAGATCTTAAAGAAAGAGGAAATGCTGAAAGAGAGAACCAAGCTTTTG	589		
Db	421	AAGCTTGTGAGATCTTAAAGAAAGAGGAAATGCTGAAAGAGAGAACCAAGCTTTTG	480		
Qy	590	GCTAGCCAGATGGAGAAATCATCATGTGGGACAGAGCTGAGATGGAGATGTCACCT	649		
Db	481	GCTAGCCAGATGGAGAAATCATCATGTGGGACAGAGCTGAGATGGAGATGTCACCT	540		
Qy	650	GCTGGACAAATCTCCGACAACTCTCCGCTGACTCTCCCACTACTTAATAGCCACCTTAA	709		
Db	541	GCTGGACAAATCTCCGACAACTCTCCGCTGACTCTCCCACTACTTAATAGCCACCTTAA	600		
Qy	710	ATCGCGGTTGAAATCAAAATCCAAAACATATATAATTAAGAGAAAAAATAAGAT	769		
Db	601	ATCGCGGTTGAAATCAAAATCCAAAACATATATAATTAAGAGAAAAAATAAGAT	660		
Qy	770	ATGTAATTTATTCGCTGATAGGGGAGCGTTTGTATCTTAATATCTCTCTCTTTGGCC	829		
Db	661	ATGTAATTTATTCGCTGATAGGGGAGCGTTTGTATCTTAATATCTCTCTCTTTGGCC	720		
Qy	830	AAGAGACTTTGTGTGATCTTAAGTAGAGCGGAACCTAAGTCAATATCTATCTGTTTAAAG	889		
Db	721	AAGAGACTTTGTGTGATCTTAAGTAGAGCGGAACCTAAGTCAATATCTATCTGTTTAAAG	780		
Qy	890	ACAAAA 895			
Db	781	ACAAAA 786			

RESULT 6  
AR476092  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

AR476092  
Sequence 1 from patent US 6693228.  
AR476092  
AR476092.1 GI:42716039  
Unknown.  
Unknown.  
Unclassified.  
1 (bases 1 to 797)  
Amasino,R.M., Schomburg,P.M., Michaels,S.D., Sung,S.-B. and

Scortecci, K.		Alteration of flowering time in plants	
Patent: US 6693228-A 1 17-FEB-2004;		Wisconsin Alumni Research Foundation; Madison, WI	
Location/Qualifiers		1..797	
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Best Local Similarity		99.9%;	Pred. No. 2.2e-233;
Matches 785;		Conservative 0;	Mismatches 1; Indels 0; Gaps 0;
Qy	110	ATGGGAAGAAAAAACTAGAAATCAAGCGAATTGAGAACAAAGTAGCGGACAAAGTCAACC	169
Db	1	ATGGGAAGAAAAAACTAGAAATCAAGCGAATTGAGAACAAAGTAGCGGACAAAGTCAACC	60
Qy	170	TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTCTGTTCTCTGTGAC	229
Db	61	TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTCTGTTCTCTGTGAC	120
Qy	230	GCATCCGTCGCTCTTCTCGTCTCTCCGCTCCGCGCAAGCTCTACAGCTTCTCTCCCGGC	289
Db	121	GCATCCGTCGCTCTTCTCGTCTCTCCGCTCCGCGCAAGCTCTACAGCTTCTCTCCCGGC	180
Qy	290	GATAACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTTAAAGCC	349
Db	181	GATAACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTTAAAGCC	240
Qy	350	TTGGATCATCATGTCAAAAGCTCTGAACTATGGTTTCACTATGAGCTACTTGAACCTTGTG	409
Db	241	TTGGATCATCATGTCAAAAGCTCTGAACTATGGTTTCACTATGAGCTACTTGAACCTTGTG	300
Qy	410	GATAGCAAGCTTTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCACACTG	469
Db	301	GATAGCAAGCTTTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCACACTG	360
Qy	470	GAGGAACACCTTGAGACTGCCCTCTCCGTGACTAGAGCCAAAGAGACCGAACTCATGTTG	529
Db	361	GAGGAACACCTTGAGACTGCCCTCTCCGTGACTAGAGCCAAAGAGACCGAACTCATGTTG	420
Qy	530	AAGCTTGTGAGAACTTTAAGAAAGAGAGAAATGCTGAAAGAGAGAACCAAGTCTTTG	589
Db	421	AAGCTTGTGAGAACTTTAAGAAAGAGAGAAATGCTGAAAGAGAGAACCAAGTCTTTG	480
Qy	590	GCTAGCCAGATGGAGAAATAATCATCATGTGGGACAGAGCTGAGATGGAGATGTCACCT	649
Db	481	GCTAGCCAGATGGAGAAATAATCATCATGTGGGACAGAGCTGAGATGGAGATGTCACCT	540
Qy	650	GCTGGACAAATCTCCGACAAATCTTCCGCTGACTCTCCCACTACTTAATAGCCACCTTAA	709
Db	541	GCTGGACAAATCTCCGACAAATCTTCCGCTGACTCTCCCACTACTTAATAGCCACCTTAA	600
Qy	710	ATCGCGGTTGAAATCAAAATCCAAAACATATATAATTAAGAGAAAAAATAAGAT	769
Db	601	ATCGCGGTTGAAATCAAAATCCAAAACATATATAATTAAGAGAAAAAATAAGAT	660
Qy	770	ATGTAATTTATTCGCTGATTAAGGGGAGCGTTTGTATCTTAATATCTCTCTTTGGCC	829
Db	661	ATGTAATTTATTCGCTGATTAAGGGGAGCGTTTGTATCTTAATATCTCTCTTTGGCC	720
Qy	830	AAGAGACTTTGTGTGATACCTTAAGTAGACGGAACTAAGTCAATATCTATCTGTTTAAAG	889
Db	721	AAGAGACTTTGTGTGATACCTTAAGTAGACGGAACTAAGTCAATATCTATCTCGTTTTAAG	780
Qy	890	ACAAAA 895	
Db	781	ACAAAA 786	
RESULT 7		AF537203	

LOCUS	AF537203	801 bp	mRNA	linear	PLN 02-SEP-2002
DEFINITION	Arabidopsis thaliana flowering locus C protein mRNA, complete cds.				
ACCESSION	AF537203				
VERSION	AF537203.1	GI:22653433			
KEYWORDS					
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
REFERENCE	1. (bases 1 to 801)				
AUTHORS	Michaelis, S.D. and Amasino, R.M.				
TITLE	FLOWERING LOCUS C encodes a novel MADS domain protein that acts as a repressor of flowering				
JOURNAL	Plant Cell 11 (5), 949-956 (1999)				
PUBMED	10330478				
REFERENCE	2. (bases 1 to 801)				
AUTHORS	Michaelis, S.D. and Amasino, R.M.				
TITLE	Direct Submission				
JOURNAL	Submitted (09-AUG-2002) Biochemistry, University of Wisconsin-Madison, 433 Babcock Drive, Madison, WI 53706, USA				
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ORIGIN					
Query Match	83.2%; Score 784.4; DB 4; Length 801;				
Best Local Similarity	99.9%; Pred. No. 2.2e-233;				
Matches	785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	110	ATGGGAAGAAAAAATCTAGAAATCAAGCGAATTGAGAACAAAGTAGCCGACAAAGTCACC	169		
DB	1	ATGGGAAGAAAAAATCTAGAAATCAAGCGAATTGAGAACAAAGTAGCCGACAAAGTCACC	60		
QY	170	TTCTCCAAACGTCGCAACGGTCTCATCGAAGAGCTCGTCAGCTTTCTCTCTGTGAC	229		
DB	61	TTCTCCAAACGTCGCAACGGTCTCATCGAAGAGCTCGTCAGCTTTCTCTCTGTGAC	120		
QY	230	GCATCGCTCGCTTCTCTGTCGTCTCGCTCCGCAAGCTCTACAGCTTCTCTCTCGGC	289		
DB	121	GCATCGCTCGCTTCTCTGTCGTCTCGCTCCGCAAGCTCTACAGCTTCTCTCTCGGC	180		
QY	290	GATAACCTGTCGAAGTCTTGTATCGATATGGAACACGATCGTATGATCTTAAAGCC	349		
DB	181	GATAACCTGTCGAAGTCTTGTATCGATATGGAACACGATCGTATGATCTTAAAGCC	240		
QY	350	TTGGATCATCAGTCAAAAGCTCTGAACTATGTTTCACTATGAGCTACTTGAACCTTGTG	409		
DB	241	TTGGATCATCAGTCAAAAGCTCTGAACTATGTTTCACTATGAGCTACTTGAACCTTGTG	300		
QY	410	GATAGCAAGCTTGTGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCAACTG	469		
DB	301	GATAGCAAGCTTGTGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCAACTG	360		
QY	470	GAGGAACACTTGTGAGACTCCCTCTCCGTGACTAGAGCCCAAGAACCACTCATGTG	529		
DB	361	GAGGAACACTTGTGAGACTCCCTCTCCGTGACTAGAGCCCAAGAACCACTCATGTG	420		
QY	530	AAGCTTTGTTGAGATCTTAAAGAAAGGAGAAAAATGCTGAAAGAGAACCAAGGTTTGTG	589		
Db	421	AGCTTTGTTGAGATCTTAAAGAAAGGAGAAAAATGCTGAAAGAGAACCAAGGTTTGTG	480		
QY	590	GCTAGCCAGATGGAGAAATATCATGTGTGGAGAGAGAGCTGAGATGGAGATGTACCT	649		
Db	481	GCTAGCCAGATGGAGAAATATCATGTGTGGAGAGAGAGCTGAGATGGAGATGTACCT	540		
QY	650	GCTGGACAAATCTCCGACAAATCTCCGGTGACTCTCCCACTACTTAAATAGCCACCTTAA	709		
Db	541	GCTGGACAAATCTCCGACAAATCTCCGGTGACTCTCCCACTACTTAAATAGCCACCTTAA	600		
QY	710	ATCGCGGTTGAAATCAAATCCAAACATATATATTAATGAGAAAAAATAAAGAT	769		
Db	601	ATCGCGGTTGAAATCAAATCCAAACATATATATTAATGAGAAAAAATAAAGAT	660		
QY	770	ATGTAATTAATTCGGCTGATAGAGCGAGCGTTTGTATATCTTAACTACTCTCTTTGGCC	829		
Db	661	ATGTAATTAATTCGGCTGATAGAGCGAGCGTTTGTATATCTTAACTACTCTCTTTGGCC	720		
QY	830	AAGAGACTTTGTGTGTACTTAAGTAGACGAACTAAAGTCAATCACTACTCTCTTTAAG	889		
Db	721	AAGAGACTTTGTGTGTACTTAAGTAGACGAACTAAAGTCAATCACTACTCTCTTTAAG	780		
QY	890	ACAAAA 895			
Db	781	ACAAAA 786			
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LOCUS	AY850001				
DEFINITION	Arabidopsis thaliana ecotype Van-0 flowering locus C protein (FLC)				
ACCESSION	AY850001				
VERSION	AY850001.1				
KEYWORDS	mRNA, complete sequence, alternatively spliced.				
ORGANISM	Arabidopsis thaliana (thale cress)				
REFERENCE	1. (bases 1 to 774)				
AUTHORS	Werner, J.D., Borevitz, J.O., Uhlenhaut, N.H., Ecker, J.R., Chory, J. and Weigel, D.				
TITLE	PRGIDA-Independent Variation in Flowering Time of Natural Arabidopsis thaliana Accessions				
JOURNAL	Genetics 170 (3), 1197-1207 (2005)				
PUBMED	15911588				
AUTHORS	Werner, J.D., Borevitz, J.O., Uhlenhaut, N.H., Ecker, J.R., Chory, J. and Weigel, D.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-DEC-2004) Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Rd., La Jolla, CA 92037, USA				
FEATURES	Location/Qualifiers				
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gene	1..774				
	/gene="FLC"				
	/note="flowering locus C protein; loss-of-function allele; contains premature stop codon in exon 6"				
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Query Match	81.7%; Score 770.8; DB 4; Length 774;				
Best Local Similarity	99.7%; Pred. No. 3.9e-229;				
Matches	772; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				









JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

allopolyploids  
Unpublished  
2 (bases 1 to 651)  
Wang,J., Tian,L., Lee,H.-S. and Chen,Z.J.  
Direct Submission  
Submitted (15-AUG-2005) Soil & Crop Sciences, Texas A&M University,  
610 Heep Center, College Station, TX 77843, USA  
Location/Qualifiers  
1..651  
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Query Match 63.0%; Score 593.8; DB 4; Length 651;  
Best Local Similarity 95.5%; Pred. No. 8.3e-174;  
Matches 622; Conservative 0; Mismatches 27; Indels 2; Gaps 1;

Qy 76 AAATTAGGGCAAAAGCCCTCTCGAG--AGAAGCCATGGGAAGAAAAAAGTGAATC 133  
Db 1 AAATTAGGGCAAAAGCCCTCTCGAGACAGAGCCATGGGAGTAAAGAACTGA 60  
Qy 134 AAGCGAATTGAGAACAAAGTAGCGGACAGTCACTTCTCCAAAGTCGCAAGCTC 193  
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Qy 254 TCCGCTCCGGCAGCTCTACAGCTTCTCTCCGGGATACCTGGTCAAGATCCTTGAT 313  
Db 181 TCCGCTCCGGCAGCTCTACAGCTTCTCTCCGGGATACCTGGTCAAGATCCTTGAT 240  
Qy 314 CGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCATGCAAGCTCTG 373  
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Qy 374 AACTATGGTTTCACTATGAGCTACTTGAACCTTGTGGATAGCAAGCTTGTGGATCAAT 433  
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Db 361 GTCAAAATGTGATATGATATGCTTGTGTTCACTGAGGAAACACCTTGGAGATCGCCCTC 420  
Qy 494 TCCGTGACTAGGCAAGAGACCGAATCTCATGTTGAGCTTGTGAGATCTTAAAGAA 553  
Db 421 TCCGTGACTAGGCAAGAGACCGAATCTCATGTTGAGCTTGTGAGATCTTAAAGAA 480  
Qy 554 AAGGAGAAATGTGAAAGAGAGAACAGGCTTTGGCTAGCCAGATGGAGATTAATCAT 613  
Db 481 AAGGAGAAATGTGAAAGAGAGAACAGGCTTTGGCTAGCCAGATGGAGATTAATCAT 540  
Qy 614 CATGTGGGACAGAGCTGAGATGGAGATGTCACCTGCTGGACAAATCTCCGACATCTT 673  
Db 541 CATGTGGGACAGAGCTGAGATGGAGATGTCACCTGCTGGACAAATCTCCGACATCTT 600  
Qy 674 CCGGTGACTCTCCCACTACTTAATTAGCCACCTTAATTCGGCGTGAAT 724

Db 601 CCGGTGACTCTCCGCTCTTAATTAGCCACCTTAATTCGGCGTGAAT 651

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LOCUS Arabidopsis thaliana isolate N1203 flowering locus C protein mRNA,  
DEFINITION complete cds.  
ACCESSION AY964092  
VERSION AY964092.1 GI:62632896  
KEYWORDS  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi  
1 (bases 1 to 591)  
Lempe,J., Balasubramanian,S., Sureshkumar,S., Singh,A., Schmid,M.  
and Weigel,D.  
Diversity of Flowering Responses in Wild Arabidopsis thaliana  
Strains  
PLoS Genet. 1 (1), E6 (2005)  
16103920  
2 (bases 1 to 591)  
Lempe,J., Balasubramanian,S., Sureshkumar,S., Singh,A., Schmid,M.  
and Weigel,D.  
Direct Submission  
Submitted (16-MAR-2005) Department of Molecular Biology, Max Planck  
Institute for Developmental Biology, Spemannstrasse 37-39, 72076  
Tuebingen, Germany  
Qualifiers  
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ORIGIN

Query Match 62.7%; Score 591; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 6.2e-173;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 170 TTCTCCAAAGCTGCCAACGCTCTCATCGAGAAAGCTCGTCAGCTTCTCTGTGAC 229  
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Qy 230 GCATCGCTGCTCTTCTGTCGTCCTCGCTCCGGCAAGCTCTACAGCTTCTCTCGGC 289  
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Qy 410 GATAGCAAGCTTGTGGATCAAAATGTCAAAATGTGAGTATCGATGCTTGTTCACATG 469

Db	301	GATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCAACTG	360
Qy	470	GAGGAACACCTTGAGACTGCCCTCTCCGTACTAGAGCCGAAGACCGAAGTCTATGTTG	529
Db	361	GAGGAACACCTTGAGACTGCCCTCTCCGTACTAGAGCCGAAGACCGAAGTCTATGTTG	420
Qy	530	AAGCTTGTGAGAACTCTTAAAGAAAGGAGAAATGCTGAAAGAGAACCAAGGTTTTC	599
Db	421	AAGCTTGTGAGAACTCTTAAAGAAAGGAGAAATGCTGAAAGAGAACCAAGGTTTTC	480
Qy	590	GCTAGCAGATGAGAAATCAATCATGTGGGAGCAGAACTGAGATGTCACTT	649
Db	481	GCTAGCAGATGAGAAATCAATCATGTGGGAGCAGAACTGAGATGTCACTT	540
Qy	650	GCTGGACAAATCTCCGACAACTCTCCGTGACTCTCCCACTACTTAATTAG	700
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DEFINITION	Arabidopsis thaliana isolate N1491 flowering locus C protein mRNA, complete cds.		
ACCESSION	AY964097		
VERSION	AY964097.1	GI:62632905	
KEYWORDS			
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
AUTHORS	Lempe, J., Balasubramanian, S., Sureshkumar, S., Singh, A., Schmid, M. and Weigel, D.		
TITLE	Diversity of Flowering Responses in Wild Arabidopsis thaliana Strains		
JOURNAL	PLOS Genet. 1 (1), B6 (2005)		
PUBMED	16103920		
REFERENCE	2 (bases 1 to 591)		
AUTHORS	Lempe, J., Balasubramanian, S., Sureshkumar, S., Singh, A., Schmid, M. and Weigel, D.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-MAR-2005) Department of Molecular Biology, Max Planck Institute for Developmental Biology, Spemannstrasse 37-39, 72076 Tuebingen, Germany		
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Query Match	62.7%; Score 591; DB 4; Length 591;		
Best Local Similarity	100.0%; Pred. No. 6.2e-173;		
Matches 591; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
Qy	110	ATGGGAGAGAAAAAATAGAAATCAAGCGAATTGAGAACAAAAGTAGCCGACAGATCACC	169
Db	1	ATGGGAGAGAAAAAATAGAAATCAAGCGAATTGAGAACAAAAGTAGCCGACAGATCACC	60

Qy	170	TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTCTGTGAC	229
Db	61	TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTCTGTGAC	120
Qy	230	GCATCCGTCCGTCTTCTCGTCCGTCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCGGC	289
Db	121	GCATCCGTCCGTCTTCTCGTCCGTCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCGGC	180
Qy	290	GATTAACCTGGTCAAGATCCTTGATCGATATGGGAAAACAGCATGCTGATGATCTTAAAGCC	349
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Qy	350	TTGGATCATCAGTCAAAAGCTCTGAACTATGGTTTCACTATGAGCTTCTTGAACCTTGTG	409
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Qy	410	GATAGCAAGCTTTGTGGGATCAAAATGTCAAAAATGTGAGTATCGATGCTCTTGTTCAACTG	469
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Qy	470	GAGGAACACCTTGAGACTGCCCTCTCCGTACTAGAGCCGAAGACCGAAGTCTATGTTG	529
Db	361	GAGGAACACCTTGAGACTGCCCTCTCCGTACTAGAGCCGAAGACCGAAGTCTATGTTG	420
Qy	530	AAGCTTGTGAGAACTCTTAAAGAAAGGAGAAATGCTGAAAGAGAACCAAGGTTTTC	599
Db	421	AAGCTTGTGAGAACTCTTAAAGAAAGGAGAAATGCTGAAAGAGAACCAAGGTTTTC	480
Qy	590	GCTAGCAGATGAGAAATCAATCATGTGGGAGCAGAACTGAGATGGAGATGTCACTT	649
Db	481	GCTAGCAGATGAGAAATCAATCATGTGGGAGCAGAACTGAGATGGAGATGTCACTT	540
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Db	541	GCTGGACAAATCTCCGACAACTCTCCGTGACTCTCCCACTACTTAATTAG	591
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LOCUS	AY964093	599 bp mRNA linear	PLN 03-AUG-2005
DEFINITION	Arabidopsis thaliana isolate N1249 flowering locus C protein mRNA, complete cds.		
ACCESSION	AY964093		
VERSION	AY964093.1	GI:62632898	
KEYWORDS			
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
AUTHORS	Lempe, J., Balasubramanian, S., Sureshkumar, S., Singh, A., Schmid, M. and Weigel, D.		
TITLE	Diversity of Flowering Responses in Wild Arabidopsis thaliana Strains		
JOURNAL	PLOS Genet. 1 (1), B6 (2005)		
PUBMED	16103920		
REFERENCE	2 (bases 1 to 599)		
AUTHORS	Lempe, J., Balasubramanian, S., Sureshkumar, S., Singh, A., Schmid, M. and Weigel, D.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-MAR-2005) Department of Molecular Biology, Max Planck Institute for Developmental Biology, Spemannstrasse 37-39, 72076 Tuebingen, Germany		
FEATURES	Location/Qualifiers		
source	1. .599		
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	/codon_start=1		

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LLVVSAGKLYSFSGDNLVKIDRYGKHADDLKALDHOSKALNYSHYELLELVDS  
KLVSNNVNSIDALVLEHLELTALSVTRAKTELMLKLVENLKEKEKMLKEENQVL  
ASQMNHHVGAEMEMSPAGQISDNLPTVLPILN"

ORIGIN

Query Match 62.7%; Score 591; DB 4; Length 599;  
Best Local Similarity 100.0%; Pred. No. 6.2e-173;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 110 ATGGGAGAGAAAACTAGAAATCAAGCGAATTGAGAACAAAGTAGCCGCAAGTCACC 169  
DB 1 ATGGGAGAGAAAACTAGAAATCAAGCGAATTGAGAACAAAGTAGCCGCAAGTCACC 60  
QY 170 TTCTCCAAAAGCTCCCAAGCGTCTCATCGAGAAAGCTCGTCAAGCTTCTGTTCTCTGTGAC 229  
DB 61 TTCTCCAAAAGCTCCCAAGCGTCTCATCGAGAAAGCTCGTCAAGCTTCTGTTCTCTGTGAC 120  
QY 230 GCATCGCTGCTTCTGCTGCTTCTGCTGCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCGCGC 289  
DB 121 GCATCGCTGCTTCTGCTGCTTCTGCTGCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCGCGC 180  
QY 290 GATTAACCTGTCAGATCTTGTGATCGATATGGAAGAACAGCATGCTGATGATCTTAAAGCC 349  
DB 181 GATTAACCTGTCAGATCTTGTGATCGATATGGAAGAACAGCATGCTGATGATCTTAAAGCC 240  
QY 350 TTGGATCATCAGTCAGAACGCTCTCAATATGTTTCAACATATGAGTACCTTGAAGCTTG 409  
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QY 410 GATAGCAAGCTTGTGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCAACTG 469  
DB 301 GATAGCAAGCTTGTGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCAACTG 360  
QY 470 GAGGAACACCTTGAGACTGCTCTCGTGAAGTGAAGCCAGAACGCAACTCATGTTG 529  
DB 361 GAGGAACACCTTGAGACTGCTCTCGTGAAGTGAAGCCAGAACGCAACTCATGTTG 420  
QY 530 AAGCTTGTGAGATCTTAAAGAAAGAGAAATGCTGAAGAAAGAGAACCGAGTTTG 589  
DB 421 AAGCTTGTGAGATCTTAAAGAAAGAGAAATGCTGAAGAAAGAGAACCGAGTTTG 480  
QY 590 GCTAGCCAGATGGAGAAATATCATCATGTGGGAGCAGAGCTGAGATGGAGATGCACCT 649  
DB 481 GCTAGCCAGATGGAGAAATATCATCATGTGGGAGCAGAGCTGAGATGGAGATGCACCT 540  
QY 650 GCTGAGCAAAATCTCCGCAAAATCTTCCGCTGACTCTCCCACTACTTAATTAG 700  
DB 541 GCTGAGCAAAATCTCCGCAAAATCTTCCGCTGACTCTCCCACTACTTAATTAG 591

RESULT 15

DQ167444  
LOCUS DQ167444  
DEFINITION Arabidopsis arenosa MADS-box flowering locus C (FLC2) mRNA, complete cds.  
VERSION DQ167444  
KEYWORDS DQ167444.1 GI:73915372  
SOURCE Arabidopsis arenosa  
ORGANISM Arabidopsis arenosa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE

Wang, J., Tian, L., Lee, H.-S. and Chen, Z.J.  
Sequence evolution, epigenetic regulation, and trans-acting effects mediate FLC expression and flowering-time variation in Arabidopsis allopolyploids  
Unpublished

REFERENCE

Wang, J., Tian, L., Lee, H.-S. and Chen, Z.J.  
Direct Submission  
JOURNAL Submitted (12-AUG-2005) Soil & Crop Sciences, Texas A&M University, 610 Heep Center, College Station, TX 77843, USA  
FEATURES Location/Qualifiers  
source 1..651  
/organism="Arabidopsis arenosa"  
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ORIGIN

Query Match 62.3%; Score 587.4; DB 4; Length 651;  
Best Local Similarity 94.9%; Pred. No. 8.3e-172;  
Matches 618; Conservative 0; Mismatches 31; Indels 2; Gaps 1;  
QY 76 AAATTAGGGCACAAAGCCCTCTCGGAG--AGAAGCCATGGAGAGAAAACTAGAATC 133  
DB 1 AAATTAGGGCACAAAGCCCTCTCGGAGACAGAGCCATGGAGAGAAAACTAGAATC 60  
QY 134 AAGCGAATTGAGAACAAAGTAGCCGACAGTCACTTCTCCAAACGTCGCAACGGTCTC 193  
DB 61 AAGCGAATTGAGAACAAAGTAGCCGACAGTCACTTCTCCAAACGTCGCAACGGTCTC 120  
QY 194 ATCGAGAAAGCTCGTCAGCTTCTGTTCTCTGTGAGCGATCCGTCGCTTCTTCGTCGTC 253  
DB 121 ATCGAGAAAGCTCGTCAGCTTCTGTTCTCTGTGAGCGATCCGTCGCTTCTTCGTCGTC 180  
QY 254 TCCGCTCCGCGCAAGCTCTACAGCTTCTCTCCGGCGATAACTGTCGATCAAGTCTTGTAT 313  
DB 181 TCTGCTTCCGCGCAAGCTCTACAGCTTCTCTCCGGCGATAACTGTCGATCAAGTCTTGTAT 240  
QY 314 CGATATGGGAAACAGCATGCTGATGATCTTAAAGCGCTTGGATCATCAGTCAAAAGCTCTG 373  
DB 241 CGATATGGGAAACAGCATGCTGATGATCTTAAAGCGCTTGGATCATCAGTCAAAAGCTCTG 300  
QY 374 AACTATGGTTTCACTATGAGCTACTTGAACTTGTGGATAGCAAGCTTGTGGATCAAAAT 433  
DB 301 AACTATGGTTTCACTATGAGCTACTTGAACTTGTGGATAGCAAGCTTGTGGATCAAAAT 360  
QY 434 GTCAAAAATGTGATGATGCTCTTGTTCATCTGAGAGAAACACTTGTGAGATGCGCCTC 493  
DB 361 GTCAAAAATGTGATGATGCTCTTGTTCATCTGAGAGAAACACTTGTGAGATGCGCCTC 420  
QY 494 TCCGTCAGTAGAGCCAGAGAGCCGAACTCATCTGTGAGCTTGTGAGATCTTAAAGAA 553  
DB 421 TCCGTCAGTAGAGCCAGAGAGCCGAACTCATCTGTGAGCTTGTGAGATCTTAAAGAA 480  
QY 554 AAGGAGAAAATGCTGAAAGAGAGAACACAGGTTTGTGCTAGCCAGATGGAGATTAATCAT 613  
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QY 614 CATGTGGAGCAGAGCTGAGATGGAGATGTCACCTGCTGGAGCAAAATCTCCGCAATCTT 673  
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QY 674 CCGGTGACTCTCCCACTACTTAAATAGCCACCTTAAATCGCGGTTGAAAT 724  
DB 601 CCGGTGACTCTCCCACTACTTAAATAGCCACCTTAAATCGCGGTTGAAAT 651

Search completed: May 22, 2006, 07:02:51  
Job time : 5456 secs

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GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2006, 05:20:17 ; Search time 645 Seconds  
(without alignments)  
10193.535 Million cell updates/sec

Title: US-09-857-346A-2  
Perfect score: 943  
Sequence: 1 cgagaaaggagaaaaaa.....tgagaaaaaa 943

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 8:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*
- 14: Geneseqn2005s:\*
- 15: Geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	943	100.0	943	10	ADD30735 Plant yie
4	943	100.0	943	12	ADI43666 Plant tra
5	943	100.0	943	12	ADO03460 Thalecres
6	784.4	83.2	797	3	AAA28120 Arabidops
7	746	79.1	758	3	AAC39385 Arabidops
8	591	62.7	591	14	AEBA7394 Arabidops
9	538.4	57.1	868	3	AAA29035 B. napus
10	528	56.0	845	3	AAA29039 B. napus
11	527	55.9	891	3	AAA29041 B. napus
12	494.8	52.5	969	3	AAA29034 B. napus
13	491.8	52.2	851	13	ADW76669 Chinese c
14	490.8	52.0	825	3	AAA29040 B. napus
15	484	51.3	990	3	AAA29037 B. napus
16	477.4	50.6	908	3	AAA29032 B. napus
17	471.4	50.0	780	3	AAA29038 B. napus
18	468.4	49.7	847	3	AAA29033 B. napus

19	454.2	49.2	792	3	AAA29036 B. napus
20	448.6	47.6	867	3	AAA28124 Brassica
21	439	46.6	863	3	AAA28123 Brassica
22	373.6	39.6	884	3	AAC38871 Arabidops
23	373.6	39.6	884	15	AEF28378 Lead_Cere
24	372.6	39.5	883	4	AAF80385 Nucleotid
25	372.6	39.5	883	10	ADD31054 Plant yie
26	372.6	39.5	883	12	ADI41552 Plant tra
27	372.6	39.5	883	12	ADO01656 Thalecres
28	372.6	39.5	883	12	ADO03320 Thalecres
29	363.8	38.6	1059	4	AAF80389 Nucleotid
30	363.8	38.6	1059	10	ADD31022 Plant yie
31	363.8	38.6	1059	12	ADI41886 Plant tra
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33	362.6	38.5	1036	10	ADO02530 Thalecres
34	362.6	38.5	1036	4	AAF80388 Nucleotid
35	362.6	38.5	1036	10	ADD31076 Plant yie
36	362.6	38.5	1036	12	ADI41702 Plant tra
37	362.6	38.5	1036	12	ADO02154 Thalecres
38	362.6	38.5	1036	12	ADO03398 Thalecres
39	360.6	38.2	604	10	ADK53672 Plant DNA
40	347	36.8	877	13	ADK45436 Plant ful
41	342	36.3	591	8	ABZ42141 Arabidops
42	339.6	36.0	610	12	ADO03536 Thalecres
43	336.6	35.7	537	10	ADK55986 Plant DNA
44	334	35.4	5968	14	AEBA7395 Arabidops
45	324.4	34.4	687	12	ADG47881 Arabidops

#### ALIGNMENTS

#### RESULT 1

AAA29031  
ID AAA29031 standard; DNA; 943 BP.

AC AAA29031;

DT 12-SEP-2000 (first entry)

DE A. thaliana flowering locus F (PLF) cDNA.

XX Flowering locus F; transcription factor; DNA binding domain; MADS box;  
XX PLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.

OS Arabidopsis thaliana.

XX Key Location/Qualifiers

FT CDS 110..700

FT /\*tag= a

FT /product= "MADS\_box\_protein"

FT /note= "encodes a transcription factor comprising a

FT distinctive DNA binding domain"

XX WO200032780-A1.

PN 08-JUN-2000.

XX 02-DEC-1999; 99WO-AU001079.

XX 03-DEC-1998; 98AU-00007469.

PR 22-JAN-1999; 99US-0116928P.

XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.

XX (PERE/) PEREZ P.

XX Perez P, Burn JE, Peacock WJ, Dennis ES, Sheldon CC;

PI Helliwell CA, Rouse DT;

XX WPI; 2000-451762/39.

DR P-PSDB; AAY96407.

XX New nucleic acid comprising a MADS box that encodes a transcription

factor for altering the flowering time or modifying the vegetative or floral phenotype of a plant such as wheat.

Claim 6; Page 83; 106pp; English.

The present cDNA, isolated from *Arabidopsis thaliana*, encodes a transcription factor protein comprising a distinct conserved DNA binding domain (a MADS box). The DNA was identified from a late-flowering mutant (C24), which arose during transformation of the early-flowering ecotype C24 with a modified binary vector pBIN-delta-Ac. This vector contains the neomycin phosphotransferase II (NPTII) gene under the control of the nopaline synthase (NOS) promoter, together with a deleted maize Ac transposable element inserted within the untranslated leader of the beta-glucuronidase gene, in the reverse orientation to the direction of transcription. It was found that two T-DNA segments segregate in the very late flowering phenotype and that two expressed genes (A and B) were closely linked to these T-DNAs. Gene B was re-designated as FLF. The FLF gene is linked to the top of chromosome 5, 4 cm from RFLP marker 447. The protein is capable of altering the flowering time of a plant. Over-expression of the FLF gene can be used to delay flowering in a plant. Alternatively, reduction of FLF gene expression, e.g. by antisense constructs, can be used to induce early flowering. Methods of modifying vegetative and/or floral phenotypes of a plant comprising increasing the level of expression of a FLF gene to modify the production or activity of a gibberellin in the plant are also claimed. The response of a plant to vernalization can also be altered. Any dicotyledonous or monocotyledonous plant species including horticultural plants, particularly those in the cut-flower industry, vegetable, cereal and other crop plants are capable of being controlled

Sequence 943 BP; 319 A; 193 C; 203 G; 228 T; 0 U; 0 Other;

Query Match 100.0%; Score 943; DB 3; Length 943;  
Best Local Similarity 100.0%; Pred No. 1.2e-240;  
Matches 943; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CGAGAAAGGAAAAAATAAGAGAGAAACGCTTAGTATCTCCGGCGACTTGAAC 60  
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DB 61 CCAACCTGAGGATCAAAATTAGGGCAAAAGCCCTCTCGAGAGAGCCATGGGAAGAA 120  
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DB 121 AAACTAGAAATCAAGCGAATTCAGAACAAAGTAGCCGACAGTCACTTCTCCAAACG 180  
QY 181 TCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTCTGTCTGTGACGCATCCGTCGC 240  
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DB 361 GTCAAAAGCTCTGAACATATGGTTTCAACATATGAGCTACTTGAACCTTGTGGATAGCAAGCT 420  
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DB 421 TGTGGATCAAAATGTCAAAATGTAGATATCGATGCTCTTGTTCATCTGGAGGAACACT 480  
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DB 481 TGAGACTGCGCTCTCCGTCAGTACAGCAAGAGACCGAACTCATGCTTGAAGCTTGTGA 540  
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DB 541 GAATCTTAAAGAAAGGAGAAATGCTGAAAGAGAGAAACAGGTTTTGGCTAGCCAGAT 600  
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DB 601 GGAGATAATCATCATGTGGAGCAGAACCTGAGATGGAGATGTCACCTGCTGGACAAAT 660  
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DB 901 ATGAACCTTTGTACCTTATTTCGTGTGAGAAAAAATAAGAAAAA 943  
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ID AAF80398 standard; cDNA; 943 BP.  
XX  
AC AAF80398;  
XX  
DT 29-JUN-2001 (first entry)  
XX  
DE Nucleotide sequence of a plant transcription factor G1759.  
KW Transcription factor; flowering time; transgenic plant; vernalisation;  
KW plant development; plant physiology; flowering; ss.  
OS *Arabidopsis thaliana*.  
FH Key Location/Qualifiers  
FT CDS 110..700  
FT /\*tag= a  
FT /product= "transcription factor"  
XX  
PN WO200126459-A2.  
XX  
PD 19-APR-2001.  
XX  
PF 11-OCT-2000; 2000WO-US028141.  
XX  
PR 12-OCT-1999; 99US-0159464P.  
PR 08-NOV-1999; 99US-0164132P.  
PR 17-NOV-1999; 99US-0166228P.  
PR 17-APR-2000; 2000US-0197899P.  
PR 22-AUG-2000; 2000US-0227439P.  
XX  
(MEND-) MENDEL BIOTECHNOLOGY INC.  
PA (RATC/) RATCLIFFE O.  
PA (HEAR/) HEARD J.  
PA (SAMA/) SAMAHA R.  
PA (CREE/) CREELMAN R.  
PA (KEDD/) KEDDIE J.  
PA (JIAN/) JIANG C.  
PA (REUB/) REUBER L.  
PA (RIEC/) RIECHMANN J L.  
XX  
PI Ratcliffe O, Heard J, Samaha R, Creelman R, Keddie J, Jiang C;  
PI Reuber L, Riechmann JL;

DR WPI; 2001-266398/27.  
DR P-PSDB; AAB67828.  
XX  
PT New transgenic plant comprises a recombinant polynucleotide encoding a  
PT plant transcription factor polypeptide and has a modified flowering time  
PT or vernalization requirement.  
XX  
PS Example 1; Page 67-68; 108pp; English.  
XX  
CC The present sequence encodes a plant transcription factor protein which  
CC modifies the flowering time of a plant. The polynucleotide sequence is  
CC used to produce transgenic plants which have a modified flowering time or  
CC a modified vernalization requirement. The polynucleotides and  
CC polypeptides are useful for modifying plant development, physiology or  
CC biochemistry such that the modified plants have a trait advantage over  
CC wild type plants. In particular they are useful for accelerating, or  
CC delaying or preventing flowering. The polynucleotides are also useful as  
CC nucleic acid probes and primers. They may be used to identify proteins  
CC that can modify the activity of the transcription factor  
XX  
SQ Sequence 943 BP; 319 A; 193 C; 203 G; 228 T; 0 U; 0 Other;  
Query Match 100.0%; Score 943; DB 4; Length 943;  
Best Local Similarity 100.0%; Pred. No. 1.2e-240;  
Matches 943; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGAGAAAGGAAAAAATAGAAAGAGAAAAAGCTTAGTATCTCCGGCGACTTGAAC 60  
Db 1 CGAGAAAGGAAAAAATAGAAAGAGAAAAAGCTTAGTATCTCCGGCGACTTGAAC 60  
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Db 61 CCAAACTGAGATCAAAATTAGGACCAAAAGCCCTCTCGAGAGAGCCATCGGAGAGAA 120  
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Db 121 AAAAAGTAAATCAAGCGAAATAGAGAAAGTAGCCGACAAAGTCACTTCTCCAAACG 180  
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Db 181 TCGAACGGTCTCATCGAGAAAGCTCGTCAAGTTTCTGTTCTCTGTGACGATCGTGGC 240  
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Db 421 TGTGGATCAATCTCAAAATGAGTATCGATGCTTCTTCTCACTGGAGGAAACCT 480  
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Db 481 TGAGACTGCCCTCTCCGTGACTAGAGCAAGACGAACTCATGTTTGAAGCTTTTGA 540  
QY 541 GAATCTTAAAGAAAGAGAAAAATGCTGAAAGAGAGAACAGAGTTTGGTACCCAGAT 600  
Db 541 GAATCTTAAAGAAAGAGAAAAATGCTGAAAGAGAGAACAGAGTTTGGTACCCAGAT 600  
QY 601 GGAGAAATCATCATGCGGAGCAGAGCTGAGATGAGATGTCACCTGCTGACAAAT 660  
Db 601 GGAGAAATCATCATGCGGAGCAGAGCTGAGATGAGATGTCACCTGCTGACAAAT 660  
QY 661 CTCGCAAACTCTCCGGTGAATCTCCCACTACTTAAATTTAGCCACTTAAATCGCGGTTG 720  
Db 661 CTCGCAAACTCTCCGGTGAATCTCCCACTACTTAAATTTAGCCACTTAAATCGCGGTTG 720

QY 721 AAATCAAAATCCAAACATATATATATATATGAAGAAAAAATAAGATATGTAATATT 780  
Db 721 AAATCAAAATCCAAACATATATATATATGAAGAAAAAATAAGATATGTAATATT 780  
QY 781 CGCTGATAAGCGGCGGCTTTGTATATCTTAAATCTCTCTCTTGGCCAGAGACTTTG 840  
Db 781 CGCTGATAAGCGGCGGCTTTGTATATCTTAAATCTCTCTCTTGGCCAGAGACTTTG 840  
QY 841 TGTGTGATCTTAACTAGTAGACGGAACCTAAGTCAATATCTGTTTAAAGCAAAAGGTTG 900  
Db 841 TGTGTGATCTTAACTAGTAGACGGAACCTAAGTCAATATCTGTTTAAAGCAAAAGGTTG 900  
QY 901 ATGAACCTTTGACCTTATTCGTGTGAGAAAAAATAAAAAA 943  
Db 901 ATGAACCTTTGACCTTATTCGTGTGAGAAAAAATAAAAAA 943  
RESULT 3  
ADD30735  
ID ADD30735 standard; cDNA; 943 BP.  
XX  
AC ADD30735;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Plant yield-related polynucleotide clone G1759.  
XX  
KW ds; transcription factor; transgenic plant; growth rate; senescence;  
KW seed germination rate; plant vigor; seedling vigor.  
XX  
OS Arabidopsis thaliana.  
XX  
FN WO2003013227-A2.  
XX  
PD 20-FEB-2003.  
XX  
PP 09-AUG-2002; 2002WO-US025805.  
XX  
PR 09-AUG-2001; 2001US-0310847P.  
PR 19-NOV-2001; 2001US-0336049P.  
PR 11-DEC-2001; 2001US-0338692P.  
PR 14-JUN-2002; 2002US-00171468.  
XX  
PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
XX  
PI Ratcliffe O, Riechmann JL, Adam LJ, Dubell AT, Heard JE;  
PI Pilgrim ML, Jiang C, Reuber TL, Creelman RA, Pineda O, Yu G;  
PI Brown PS;  
XX  
WPI; 2003-248221/24.  
DR P-PSDB; ADD30736.  
XX  
PT New plant transcription factor polynucleotides and polypeptides, useful  
PT in producing transgenic plants with commercially valuable properties,  
PT such as an alteration in a plant growth characteristic, e.g. growth rate  
PT or apomixis.  
XX  
PS Disclosure; SEQ ID NO 764; 454pp; English.  
XX  
CC The invention relates to a number of isolated Arabidopsis thaliana cDNA  
CC sequences and their encoded proteins which are especially transcription  
CC factor related cDNA's and proteins. The isolated or recombinant plant  
CC transcription factor polynucleotides and polypeptides are useful in  
CC producing transgenic plants with commercially valuable properties, i.e.  
CC modified or altered desirable traits as compared to a reference plant,  
CC such as an alteration in a plant growth characteristic, e.g. growth rate,  
CC germination rate of seeds, vigor of plants and seedlings, or leaf and  
CC flower senescence. Sequence information related to the polynucleotides  
CC and polypeptides can also be used in bioinformatic search methods. The  
CC transgenic plant is useful for growing a progeny plant from a parent  
CC plant. This sequence represents one of the cDNAs of the invention.  
XX



SQL Sequence 943 BP; 319 A; 193 C; 203 G; 228 T; 0 U; 0 Other;

Query Match 100.0%; Score 943; DB 10; Length 943;  
Best Local Similarity 100.0%; Pred. No. 1.2e-240;  
Matches 943; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CGAGAAAGGAAAAAATAGAAAGAGAAACGCTTAGTATCTCCGGCGACTTGAAC 60
Db 1 CGAGAAAGGAAAAAATAGAAAGAGAAACGCTTAGTATCTCCGGCGACTTGAAC 60
Qy 61 CCAAACTGAGGATCAAAATAGGGCAAAAGCCCTCTCGAGAGAGCCATGGAGAA 120
Db 61 CCAAACTGAGGATCAAAATAGGGCAAAAGCCCTCTCGAGAGAGCCATGGAGAA 120
Qy 121 AAACTAGAAATCAAGCGAATTCGAGACAAAGTAGCGGACAGTCACTTCTCCAAACG 180
Db 121 AAACTAGAAATCAAGCGAATTCGAGACAAAGTAGCGGACAGTCACTTCTCCAAACG 180
Qy 181 TCGCAACGGTCTCATTCGAGAAAGCTGGTCAAGCTTTCTGTCTGTGAAGCATCCGTCGC 240
Db 181 TCGCAACGGTCTCATTCGAGAAAGCTGGTCAAGCTTTCTGTCTGTGAAGCATCCGTCGC 240
Qy 241 TCTTCTCGTGTCTCCGCTCCGGCAAGCTCTACAGCTTCTCCGGCGAATACCTGGT 300
Db 241 TCTTCTCGTGTCTCCGCTCCGGCAAGCTCTACAGCTTCTCCGGCGAATACCTGGT 300
Qy 301 CAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCA 360
Db 301 CAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCA 360
Qy 361 GTCAAAGCTCTGAACTATGGTTCACTATGAGCTACTTGAACCTTGTGATAGCAAGCT 420
Db 361 GTCAAAGCTCTGAACTATGGTTCACTATGAGCTACTTGAACCTTGTGATAGCAAGCT 420
Qy 421 TGTGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTGTTCACTGAGGAAACACCT 480
Db 421 TGTGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTGTTCACTGAGGAAACACCT 480
Qy 481 TGAGACTGCCCTCTCCGTGACTAGCCAGAGAGCCGAACTCATCTTGAAGCTTGTGA 540
Db 481 TGAGACTGCCCTCTCCGTGACTAGCCAGAGAGCCGAACTCATCTTGAAGCTTGTGA 540
Qy 541 GAATCTTAAAGAAAGGAGAAATGCTGAAAGAGAGAACCGAGTTTGGCTAGCCAGAT 600
Db 541 GAATCTTAAAGAAAGGAGAAATGCTGAAAGAGAGAACCGAGTTTGGCTAGCCAGAT 600
Qy 601 GGAGAAATATCATCATGTGGGAGCAGAGCTGAGATGAGATGTCACCTGCTGGACAAAT 660
Db 601 GGAGAAATATCATCATGTGGGAGCAGAGCTGAGATGAGATGTCACCTGCTGGACAAAT 660
Qy 661 CTCGGACAATCTTCGGGTGACTCTCCCACTACTTAATTAGCCACCTTAATCGCGGTG 720
Db 661 CTCGGACAATCTTCGGGTGACTCTCCCACTACTTAATTAGCCACCTTAATCGCGGTG 720
Qy 721 AAATCAAAATCCAAACATATATAATTAAGAAAAAATAAGATATGTAATATT 780
Db 721 AAATCAAAATCCAAACATATATAATTAAGAAAAAATAAGATATGTAATATT 780
Qy 781 CGCTGATAGGGCGAGGTTGTATATCTTAATATCTCTCTTTGGCCAAAGAGACTTGG 840
Db 781 CGCTGATAGGGCGAGGTTGTATATCTTAATATCTCTCTTTGGCCAAAGAGACTTGG 840
Qy 841 TGTGTACTACTTAAGTAGCGGAACTAAGTCAATCTCTGTTTAAAGCAAAAGGTTG 900
Db 841 TGTGTACTACTTAAGTAGCGGAACTAAGTCAATCTCTGTTTAAAGCAAAAGGTTG 900
Qy 901 ATGAACCTTTGACTTATTCGTGTGAGAAAAAATAAAAAA 943
Db 901 ATGAACCTTTGACTTATTCGTGTGAGAAAAAATAAAAAA 943
```

RESULT 4  
ADI43666

```
ID XX ADI43666 standard; DNA; 943 BP.
AC XX ADI43666;
XX XX 22-APR-2004 (first entry)
DT XX Plant transcription factor polynucleotide #1424.
DE XX
XX XX transgenic; plant; enhanced tolerance to abiotic stress;
KW glycosphate tolerance; hormone sensitivity; disease resistance;
KW sugar sensing; flowering; flower structure; stem bifurcation;
KW branching pattern; apical dominance; trichome; stem morphology;
KW root growth; root hair; seed development; cell proliferation;
KW cell differentiation; premature senescence; necrosis; plant size;
KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
KW plant anthocyanin; light response; shade avoidance; bioinformatic;
KW transcription factor; gene; ds.
XX XX Arabidopsis thaliana.
XX XX US2004019927-A1.
XX XX 29-JAN-2004.
XX XX 25-FEB-2003; 2003US-00374780.
XX XX 18-APR-2001; 2001US-00837944.
XX XX (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J B.
PA (HAAR/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
XX XX Sherman BK, Riechmann JB, Jiang C, Heard JB, Haake V;
PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Reddie J, Broun PE;
PI Pilgrim ML, Dubell AN, Pineda O, Yu G;
XX XX WPI; 2004-132245/13.
XX XX New transgenic plant comprising a recombinant polynucleotide of any one
PT of more than 500 nucleotide sequences, useful in bioinformatic search
PT methods.
XX XX Claim 1; SEQ ID NO 2129; 435pp; English.
XX XX The invention describes a transgenic plant comprising a recombinant
CC polynucleotide of any one of more than 500 nucleotide sequences fully
CC defined in the specification or its complement. The method of the
CC invention can be used to produce a plant having altered traits such as:
CC enhanced tolerance to abiotic stress; glycosphate tolerance; hormone
CC sensitivity; disease resistance; sugar sensing; early or late flowering;
CC altered flower structure; change in stem bifurcations; altered branching
CC pattern; reduced apical dominance; reduced trichome density; lack of
CC trichomes; reduced ectopic trichome development; altered trichome
CC development; increase in trichome number; altered stem morphology;
CC increased root growth; increased root hairs; altered seed development;
CC altered cell proliferation or cell differentiation; rapid development;
CC premature senescence; increased necrosis; increase in seedling or plant
CC size; decreased plant size; leaf morphology; seed morphology; seed
CC biochemistry; increase in root anthocyanins; increase in plant
CC anthocyanins, or alteration in light response or shade avoidance. The
CC transgenic plant, polynucleotides and polypeptides are useful in
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CC	bioinformatic search methods. This sequence represents a plant									
CC	transcription factor, and an orthologue of Arabidopsis thaliana									
CC	transcription factors isolated in the invention, that can be used in the									
CC	creation of a transgenic plant with altered traits.									
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OS	Arabidopsis thaliana.	
XX	Key	Location/Qualifiers
XX	PH	1..591
FT	CDS	/tag= a
FT		/product= "FLC1"
FT		/note= "Flowering locus C 1 protein"
XX		
XX	W0200050615-A1.	
XX		
XX	31-AUG-2000.	
XX		
XX	25-FEB-2000; 2000WO-US004940.	
XX		
XX	25-FEB-1999; 99US-0121572P.	
PR	09-MAR-1999; 99US-0123455P.	
XX		
XX	(WISC ) WISCONSIN ALUMNI RES FOUND.	
PA		
XX	Amasino RM, Schomburg PM, Michaels SD, Sung S, Scortecci K;	
PI		
XX	WPI; 2000-533182/48.	
DR	P-PSDB; AAY94703.	
XX		
XX	New transgenic plant with altered flowering time has a transgene for a	
XX	member of the flowering locus C gene family in its genome.	
XX		
XX	Claim 12; Page 36-37; 56pp; English.	
XX		
CC	This invention relates to a transgenic plant that comprises in its genome a transgene encoding a member of the flowering locus C (FLC) gene family. The transgenic plant has an altered timing of its flowering time compared to non-transgenic plants of the same species. The invention includes a seed of the transgenic plant which contains a plant expressible promoter and a protein coding region for a plant FLC protein which has a MADS box domain, and is effective at causing a delay in flowering time when expressed in a plant. FLC genes are MADS box genes. The MADS box is a highly conserved motif shared by a group of transcription factors. The methods of the invention are used to produce transgenic plants with altered flowering characteristics compared to flowering plants of the same species. Altering the flowering time allows the vegetative growth or flower creation by a plant to be increased, depending on the type of plant and the needs of the plant breeder. Transgenic plants which can be produced include monocotyledons e.g. asparagus, onions, maize, barley and turf grasses and dicotyledonous plants e.g. tomato, beans, cotton, flowers and shrubs. The methods disclosed in the invention allow the flowering time of the transgenic plant to be altered in either direction when compared to the wild-type plant. The present sequence represents Arabidopsis thaliana cDNA encoding the FLC1 protein. The cDNA and protein sequences are used in the construction of the transgenic plant of the invention	
XX		
XX	Sequence 797 BP; 261 A; 167 C; 169 G; 200 T; 0 U; 0 Other;	
SQ		
	Query Match	83.2%; Score 784.4; DB 3; Length 797;
	Best Local Similarity	99.9%; Pred. No. 2.1e-198;
	Matches 785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	110	ATGGGAGAGAAAACTAGAAATCAAGCAATTCAGCAACAAAGTAGCCGACAGTCACC 169
Db	1	ATGGGAGAGAAAAAATAGAAATCAAGCAATTCAGCAACAAAGTAGCCGACAGTCACC 60
Qy	170	TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTCTCTGTGAC 229
Db	61	TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTCTCTGTGAC 120
Qy	230	GCATCCGTCCTCTTCTCGTCTCCGCTCCGCGAAGCTCTACAGCTTCTCTCCGGC 289
Db	121	GCATCCGTCCTCTTCTCGTCTCCGCTCCGCGAAGCTCTACAGCTTCTCTCCGGC 180
Qy	290	GATAACCTGGTCAAGATCCCTTGTATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCC 349
Db	181	GATAACCTGGTCAAGATCCCTTGTATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCC 240

Qy	350	TTGGATCATAGTCAAAAAGCTCTGAACTATAGTTTCACTATGAGCTACTTGAACCTTGTG 409
Db	241	TTGGATCATAGTCAAAAAGCTCTGAACTATAGTTTCACTATGAGCTACTTGAACCTTGTG 300
Qy	410	GATAGCAAGCTTGTGGGATCAAAATGTCAAAAATGTGAGTATCGATGCTCTTGTTCACATG 469
Db	301	GATAGCAAGCTTGTGGGATCAAAATGTCAAAAATGTGAGTATCGATGCTCTTGTTCACATG 360
Qy	470	GAGGAACACCTTGTGAGACTGCGCTCTCCGTGACTAGAGCCAAAGAACGCAACTCAATGTTG 529
Db	361	GAGGAACACCTTGTGAGACTGCGCTCTCCGTGACTAGAGCCAAAGAACGCAACTCAATGTTG 420
Qy	530	AAGCTTGTGAGAAATCTTAAAGAAAGGAGAAAAATGCTGAAAGAGAGAACCAAGGTTTGTG 589
Db	421	AAGCTTGTGAGAAATCTTAAAGAAAGGAGAAAAATGCTGAAAGAGAGAACCAAGGTTTGTG 480
Qy	590	GCTAGCCAGATGGAGAAATATCATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACCT 649
Db	481	GCTAGCCAGATGGAGAAATATCATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACCT 540
Qy	650	GCTGACAAATCTCCGACAAATCTTCCGTGACTCTCCGACTACTTAAATTAGCCACCTTAA 709
Db	541	GCTGACAAATCTCCGACAAATCTTCCGTGACTCTCCGACTACTTAAATTAGCCACCTTAA 600
Qy	710	ATCGGCGTTGAAATCAAAATCCAAATCATATATAATTAATGAGAAAAAATAAGAT 769
Db	601	ATCGGCGTTGAAATCAAAATCCAAATCATATATAATTAATGAGAAAAAATAAGAT 660
Qy	770	ATGTAATTTTCCGCTGATAGGGGAGCGGTTGTATATCTTAATACTCTCTCTTTGGCC 829
Db	661	ATGTAATTTTCCGCTGATAGGGGAGCGGTTGTATATCTTAATACTCTCTCTTTGGCC 720
Qy	830	AAGAGACTTTGTGTGTATCTTAAGTAGAGCGAACTAAGTCAATACTATCTGTTTTAAG 889
Db	721	AAGAGACTTTGTGTGTATCTTAAGTAGAGCGAACTAAGTCAATACTATCTGTTTTAAG 780
Qy	890	ACAAAA 895
Db	781	ACAAAA 786
XX		
XX	RESULT 7	
XX	AAC39385	
ID	AAC39385	standard; DNA; 758 BP.
AC	AAC39385;	
XX	17-OCT-2000	(first entry)
DE	Arabidopsis thaliana	DNA fragment SEQ ID NO: 24438.
XX	Hybridisation assay; genetic mapping; gene expression control;	
XX	protein identification; signal transduction pathway; metabolic pathway;	
XX	promoter; termination sequence; ss.	
XX	Arabidopsis thaliana.	
XX	EP1033405-A2.	
XX	06-SEP-2000.	
XX	25-FEB-2000; 2000EP-00301439.	
XX	25-FEB-1999; 99US-0121825P.	
XX	05-MAR-1999; 99US-0123180P.	
XX	09-MAR-1999; 99US-0123548P.	
XX	23-MAR-1999; 99US-0125788P.	
XX	25-MAR-1999; 99US-0126264P.	
XX	29-MAR-1999; 99US-0126785P.	
XX	01-APR-1999; 99US-0127462P.	
XX	08-APR-1999; 99US-0128234P.	
XX	08-APR-1999; 99US-0128714P.	

PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
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PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
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PR 14-MAY-1999; 99US-0134219P.  
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PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135829P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
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PR 18-JUN-1999; 99US-0139458P.  
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PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
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PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
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PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
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PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.

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PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
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PR 21-JUL-1999; 99US-0144814P.  
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PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
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PR	25-OCT-1999;	99US-0161404P.
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Best Local Similarity 79.1%; Score 746; DB 3; Length 758;

Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Qy	302	AAGATCCTTGATCGATATGGGAAACAGCATGCTCATGATCTTTAAAGCCTTGGATCATCAG	361
Db	313	AAGATCCTTGATCGATATGGGAAACAGCATGCTCATGATCTTTAAAGCCTTGGATCATCAG	372
Qy	362	TCAAAAGCTCTGAACATATGGTTCACTATGAGCTACTTTGAACCTTTGGATAGCAAGCTT	421
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Qy	482	GAGACTCCCTCTCCGTGACTAGAGCCAAAGAACCGAATCAATGTTGTAAGCTTTGTGAG	541
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Qy	602	GAGATTAATCATATGTGGGAGCAAGAGCTGAGATGAGATGTCACTGTCTGGCAAAATC	661
Db	613	GAGATTAATCATATGTGGGAGCAAGAGCTGAGATGAGATGTCACTGTCTGGCAAAATC	672

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QY 410 GATAGCAAGCTTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTTGTTCACACTG 469
Db 301 GATAGCAAGCTTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTTGTTCACACTG 360
QY 470 GAGGACACCTTCGAGCTGCCCTCTCGTCACTAGAGCCCAAGAGACCGAATCATGTTG 529
Db 361 GAGGACACCTTCGAGCTGCCCTCTCGTCACTAGAGCCCAAGAGACCGAATCATGTTG 420
QY 530 AAGCTTGTTCAGAAATCTTAAAGAAAAGGAGAAAATGCTGAAAGAGAGAACACCGTGTG 589
Db 421 AAGCTTGTTCAGAAATCTTAAAGAAAAGGAGAAAATGCTGAAAGAGAGAACACCGTGTG 480
QY 590 GCTAGCCAGATGAGAAATATCATATGCTGGGAGCAGAACTGAGATGGAGATGTCACT 649
Db 481 GCTAGCCAGATGAGAAATATCATATGCTGGGAGCAGAACTGAGATGGAGATGTCACT 540
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RESULT 9
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AC AAA29035;
DT
DT 12-SEP-2000 (first entry)
XX
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XX
KW Flowering locus F; transcription factor; DNA binding domain; MADS box;
KW FLP; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.
XX
OS Brassica napus.
XX
Key Location/Qualifiers
FT 80..673
CDS /*tag= a
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FT
FT
XX WO200032780-A1.
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PD 08-JUN-2000.
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PF 02-DEC-1999; 99WO-AU001079.
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PF 03-DEC-1998; 98AU-00007469.
XX
PR 22-JAN-1999; 99US-0116928P.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
PA (PERE/) PEREZ P.
XX
XX Perez P, Burn JE, Peacock WJ, Dennis ES, Sheldon CC;
PI Helliwell CA, Rouse DT;
XX
XX WPI; 2000-451762/39.
XX
XX P-PSDB; AAY96411.
XX
XX New nucleic acid comprising a MADS box that encodes a transcription
PT factor for altering the flowering time or modifying the vegetative or
PT floral phenotype of a plant such as wheat.
XX
XX Claim 6; Page 87-88; 106pp; English.
XX
XX AAA29032-41 are cDNA clones isolated from a Brassica napus cDNA library
CC using hybridisation to an FLP (flowering locus F) cDNA from Arabidopsis
CC thaliana. From both amino acid and nucleotide sequence data it was
CC concluded that the clones represent transcripts from 5 different genes.
CC
```

The FLP gene encodes a transcription factor protein comprising a distinctive conserved DNA binding domain (a MADS box). The DNA was identified from a late-flowering mutant (flf), which arose during transformation of the early-flowering ecotype C24 with a modified binary vector pBin-delta-Ac. It was found that two T-DNAs segregate in the very late flowering phenotype and that two expressed genes (A and B) were closely linked to these T-DNAs. Gene B was re-designated as FLP. The FLP gene is linked to the top of chromosome 5, 4 cm from RFLP marker 447. The protein is capable of altering the flowering time of a plant. Over-expression of the FLP gene can be used to delay flowering in a plant. Alternatively, reduction of FLP gene expression, e.g. by antisense constructs, can be used to induce early flowering. Methods of modifying the level of expression of a FLP gene to modify the production or activity of a gibberellin in the plant are also claimed. The response of a plant to vernalization can also be altered. Any dicotyledonous or monocotyledonous plant species including horticultural plants, particularly those in the cut-flower industry, vegetable, cereal and other crop plants are capable of being controlled

Sequence 868 BP; 273 A; 187 C; 196 G; 212 T; 0 U; 0 Other;

Query Match 57.1%; Score 538.4; DB 3; Length 868;  
Best Local Similarity 81.7%; Pred. No. 7.4e-133;  
Matches 688; Conservative 0; Mismatches 136; Indels 18; Gaps 5;

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QY 93 CCTCTCGGAG--AGAAAGCCATGGGAAGAAAAAATAGAAAAATCAAGCGAATTTGAGAACAA 150
Db 61 ACTGTTGGAGACAGAAAGCCATGGGAGGAAGAAACTTGAATTCAGCGAATTTGAGAACAA 120
QY 151 AAGTAGCCGACAAGTCACCTTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCA 210
Db 121 AAGTAGCCGACAAGTTACCTTCTTAAACGACGCAACGGTCTCATCGAGAAAGCTCGTCA 180
QY 211 GCTTTCTGTTCTGTGACGCATCCGTCGCTCTTCTCGTCGTCCTCCGCTCCGGCAAGCT 270
Db 181 GCTTTCCGTTCTGTGACGCATCCGTCGCTCTTCTGTGTCCTCCGCTCCGGGAAACT 240
QY 271 CTACAGCTTCTCTCCGCGGATAAACCCTGGTCAAGATCCTTGATCGATATGGGAAACAGCA 330
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QY 331 TGCTGATGATCTTAAAGCCTTGGATCATCAGTCAAAAGCTCTGAACTATGTTTCACTA 390
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Db 361 TGAGCTACTTGAACCTTGGATAGCAAGCTTGGGATCAAAATGTCAAAATGTGAGTAT 420
QY 451 CGATGCTCTTGTTCACCTCGGAGAACACCTTCGAGACTGCCCTCTCCGTCAGCTAGAGCCAA 510
Db 421 GGGTTCCTGTTTCAGCTGGAGAACACCTTCGAGAACGCCCTCTCCGTAACAGAGCTAG 480
QY 511 GAAGACCGAATCATGTTGAGCTTGTGAGAACTTTAAAGAAAGAGAGAAATGCTGAA 570
Db 481 GAAGACAGAACTAATGTTGAGCTTGTGAGAACTTTAAAGAAAGAGAGAAATGCTGGA 540
QY 571 AGAAGAGAACGAGTTTGGCTAGCAGATGAGAAATATCATATGTTGGGAGCAGAAC 630
Db 541 AGAGAGAACCACTGTTTGGCTAGCAGATGAGAAAGAGTAAATCTTGTGCGAGCCGAAGC 600
QY 631 TGAGATGGAGATGTCACTGCTGGGCAAAATCTCCGA---CAATCTTCCGTCAGCTCTCCC 687
Db 601 TGATTAATGATGTCTCACAGGACAAATCTCCGACATCAATCTTCCGTAACGCTCCC 660
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Db 661 ACTGCTTAATTAGTCACCTTTAATCGGCAAT--AAATAAAATCCAAAACATAT----- 712
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XX	AC	AAA29041;	
XX	DT	12-SEP-2000 (first entry)	
XX	DE	B. napus flowering locus F (FLF) homologous cDNA 10.	
XX	KW	Flowering locus F; transcription factor; DNA binding domain; MADS box;	
XX	KW	FLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.	
XX	OS	Brassica napus.	
XX	XX	Key	Location/Qualifiers
XX	XX	CD5	67..660
XX	XX	FT	/*tag= a
XX	XX	FT	/product= "FLF_homologue"
XX	XX	PN	WO200032780-A1.
XX	XX	PD	08-JUN-2000.
XX	XX	PF	02-DEC-1999; 99WO-AU001079.
XX	XX	PR	03-DEC-1998; 98AU-00007469.
XX	XX	PR	22-JAN-1999; 99US-0116928P.
XX	XX	XX	(CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX	XX	PA	(PERE/) PEREZ P.
XX	XX	PI	Perez P, Burn JE, Peacock WJ, Dennis ES, Sheldon CC;
XX	XX	PI	Helliwell CA, Rouse DT;
XX	XX	XX	WPI; 2000-451762/39.
XX	XX	DR	P-PSDB; AAY96417.
XX	XX	XX	New nucleic acid comprising a MADS box that encodes a transcription
XX	XX	PT	factor for altering the flowering time or modifying the vegetative or
XX	XX	PT	floral phenotype of a plant such as wheat.
XX	XX	PS	Claim 6; Page 90-91; 106pp; English.
XX	XX	XX	AAA29032-41 are cDNA clones isolated from a Brassica napus cDNA library
XX	XX	CC	using hybridisation to an FLF (flowering locus F) cDNA from Arabidopsis
XX	XX	CC	thaliana. From both amino acid and nucleotide sequence data it was
XX	XX	CC	concluded that the clones represent transcripts from 5 different genes.
XX	XX	CC	The FLF gene encodes a transcription factor protein comprising a
XX	XX	CC	distinctive conserved DNA binding domain (a MADS box). The DNA was
XX	XX	CC	identified from a late-flowering mutant (elf), which arose during
XX	XX	CC	transformation of the early-flowering ecotype C24 with a modified binary
XX	XX	CC	vector pBin-delta-Ac. It was found that two T-DNAs segregate in the very
XX	XX	CC	late flowering phenotype and that two expressed genes (A and B) were
XX	XX	CC	closely linked to these T-DNAs. Gene B was re-designated as FLF. The FLF
XX	XX	CC	gene is linked to the top of chromosome 5, 4 cm from RFLP marker 447. The
XX	XX	CC	protein is capable of altering the flowering time of a plant. Over-
XX	XX	CC	expression of the FLF gene can be used to delay flowering in a plant.
XX	XX	CC	Alternatively, reduction of FLF gene expression, e.g. by antisense
XX	XX	CC	constructs, can be used to induce early flowering. Methods of modifying
XX	XX	CC	vegetative and/or floral phenotypes of a plant comprising increasing the
XX	XX	CC	level of expression of a FLF gene to modify the production or activity of
XX	XX	CC	a gibberellin in the plant are also claimed. The response of a plant to
XX	XX	CC	vernalization can also be altered. Any dicotyledonous or monocotyledonous
XX	XX	CC	plant species including horticultural plants, particularly those in the
XX	XX	CC	cut-flower industry, vegetable, cereal and other crop plants are capable
XX	XX	CC	of being controlled
XX	XX	XX	Sequence 891 BP; 276 A; 191 C; 202 G; 222 T; 0 U; 0 Other;
XX	XX	XX	Query Match 55.9%; Score 527; DB 3; Length 891;
XX	XX	XX	Best Local Similarity 81.5%; Pred. No. 8.2e-130;
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XX	XX	KW	Flowering locus F; transcription factor; DNA binding domain; MADS box;
XX	XX	KW	FLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.
XX	XX	OS	Brassica napus.
XX	XX	XX	Key
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QY	ID	AAA29034	standard; cDNA; 969 BP.
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XX	XX	OS	Brassica napus.
XX	XX	XX	Key
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XX	XX	OS	Brassica napus.
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XX	XX	OS	Brassica napus.
XX	XX	XX	Key
XX	XX	XX	Location/Qualifiers
QY	ID	AAA29034	standard; cDNA; 969 BP.
XX	AC	AAA29034;	
XX	DT	12-SEP-2000 (first entry)	
XX	XX	DE	B. napus flowering locus F (FLF) homologous cDNA 3.
XX	XX	KW	Flowering locus F; transcription factor; DNA binding domain; MADS box;
XX	XX	KW	FLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.
XX	XX	OS	Brassica napus.
XX	XX	XX	Key
XX	XX	XX	Location/Qualifiers
QY	ID	AAA29034	standard; cDNA; 969 BP.
XX	AC	AAA29034;	
XX	DT	12-SEP-2000 (first entry)	
XX	XX	DE	B. napus flowering locus F (FLF) homologous cDNA 3.
XX	XX	KW	Flowering locus F; transcription factor; DNA binding domain; MADS box;
XX	XX	KW	FLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.
XX	XX	OS	Brassica napus.
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XX	XX	KW	FLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.
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XX	XX	KW	FLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.
XX	XX	OS	Brassica napus.
XX	XX	XX	Key
XX	XX	XX	Location/Qualifiers
QY	ID	AAA29034	standard; cDNA; 969 BP.
XX	AC	AAA29034;	
XX	DT	12-SEP-2000 (first entry)	
XX	XX	DE	B. napus flowering locus F (FLF) homologous cDNA 3.
XX	XX	KW	Flowering locus F; transcription factor; DNA binding domain; MADS box;
XX	XX	KW	FLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.
XX	XX	OS	Brassica napus.
XX	XX	XX	Key
XX	XX	XX	Location/Qualifiers
QY	ID	AAA29034	standard; cDNA; 969 BP.
XX	AC	AAA29034;	
XX	DT	12-SEP-2000 (first entry)	
XX	XX	DE	B. napus flowering locus F (FLF) homologous cDNA 3.
XX	XX	KW	Flowering locus F; transcription factor; DNA binding domain; MADS box;
XX	XX	KW	FLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.
XX	XX	OS	Brassica napus.
XX	XX	XX	Key
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XX	XX	KW	FLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.
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XX	XX	KW	Flowering locus F; transcription factor; DNA binding domain; MADS box;
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XX	XX	XX	Location/Qualifiers
QY	ID	AAA29034	standard; cDNA; 969 BP.
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XX	XX	DE	B. napus flowering locus F (FLF) homologous cDNA 3.
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XX	XX	KW	FLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.
XX	XX	OS	Brassica napus.
XX	XX	XX	Key
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XX	XX	DE	B. napus flowering locus F (FLF) homologous cDNA 3.
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XX	XX	OS	Brassica napus.
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QY	ID	AAA29034	standard; cDNA; 969 BP.
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XX	XX	KW	Flowering locus F; transcription factor; DNA binding domain; MADS box;
XX	XX	KW	FLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.
XX	XX	OS	Brassica napus.
XX	XX	XX	Key
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QY	ID	AAA29034	standard; cDNA; 969 BP.
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XX	XX	DE	B. napus flowering locus F (FLF) homologous cDNA 3.
XX	XX	KW	Flowering locus F; transcription factor; DNA binding domain; MADS box;
XX	XX	KW	FLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.
XX	XX	OS	Brassica napus.
XX	XX	XX	Key
XX	XX	XX	Location/Qualifiers
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XX	XX	KW	Flowering locus F; transcription factor; DNA binding domain; MADS box;
XX	XX	KW	FLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.
XX	XX	OS	Brassica napus.
XX	XX	XX	Key
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XX	XX	KW	Flowering locus F; transcription factor; DNA binding domain; MADS box;
XX	XX	KW	FLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.
XX	XX	OS	Brassica napus.
XX	XX	XX	Key
XX	XX	XX	Location/Qualifiers
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XX	XX	KW	FLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.
XX	XX	OS	Brassica napus.
XX	XX	XX	Key
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 XX WO200032780-A1.  
 XX 08-JUN-2000.  
 XX 02-DEC-1999; 99WO-AU001079.  
 XX 03-DEC-1998; 98AU-00007469.  
 PR 22-JAN-1999; 99US-0116928P.  
 XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 PA (PERE/) PEREZ P.  
 XX Perez P, Burn JE, Peacock WJ, Dennis ES, Sheldon CC;  
 PI Helliwell CA, Rouse DT;  
 XX WPI; 2000-451762/39.  
 DR P-PSDB; AAY96410.  
 XX  
 XX New nucleic acid comprising a MADS box that encodes a transcription  
 PT factor for altering the flowering time or modifying the vegetative or  
 PT floral phenotype of a plant such as wheat.  
 XX  
 PS Claim 6; Page 87; 106pp; English.  
 XX  
 CC AAA29032-41 are cDNA clones isolated from a Brassica napus cDNA library  
 CC using hybridisation to an FLF (flowering locus P) cDNA from Arabidopsis  
 CC thaliana. From both amino acid and nucleotide sequence data it was  
 CC concluded that the clones represent transcripts from 5 different genes.  
 CC The FLF gene encodes a transcription factor protein comprising a  
 CC distinctive conserved DNA binding domain (a MADS box). The DNA was  
 CC identified from a late-flowering mutant (flf), which arose during  
 CC transformation of the early-flowering ecotype C24 with a modified binary  
 CC vector pbin-delta-3c. It was found that two T-DNAs segregate in the very  
 CC late flowering phenotype and that two expressed genes (A and B) were  
 CC closely linked to these T-DNAs. Gene B was re-designated as FLF. The FLF  
 CC gene is linked to the top of chromosome 5, 4 cm from RFLP marker 447. The  
 CC protein is capable of altering the flowering time of a plant. Over-  
 CC expression of the FLF gene can be used to delay flowering in a plant.  
 CC Alternatively, reduction of FLF gene expression, e.g. by antisense  
 CC constructs, can be used to induce early flowering. Methods of modifying  
 CC vegetative and/or floral phenotypes of a plant comprising increasing the  
 CC level of expression of a FLF gene to modify the production or activity of  
 CC a gibberellin in the plant are also claimed. The response of a plant to  
 CC vernalization can also be altered. Any dicotyledonous or monocotyledonous  
 CC plant species including horticultural plants, particularly those in the  
 CC cut-flower industry, vegetable, cereal and other crop plants are capable  
 CC of being controlled  
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 Best Local Similarity 80.66; Pred. No. 3.2e-121;  
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 DT 24-MAR-2005 (first entry)  
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 PA  
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Matches 587; Conservative 0; Mismatches 97; Indels 8; Gaps 3;		
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Qy	108 CCATGGGAAGAAATAAATAGAAATCAAGCGAATTTGCAACAAAGTAGCGGACGAAGTCA 167	
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Qy	168 CTTTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTCTCTCTGTG 227	
Db	125 CTTTCTCCAAACGAGCAATGGTCTCATCGAGAAAGCTCGTCAGCTTTCACTTCTCTGCG 184	
Qy	228 ACGATCGTCTGCTTCTCTGCTGCTCGGCTCGGCAAGCTCTACAGCTTCTCTCTCCG 287	
Db	185 ATGATCGTCTGCTTCTCTGCTGCTCGGCTCGGCAAGCTTTACAACCTTCTCTCGCG 244	
Qy	288 GCGATACTGCTCAAGATCTTGCATGATATGGAAACAGCATGCTGATGATCTTAAAG 347	
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Qy	348 CTTTGGATCATCAGTCAAAAGCTCTGAACTATGGTTTCACTATGAGCTACTTGAACCTTG 407	
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Qy	408 TGGATAGCAAGCTTGTGGATCAAAATGTCAAAAATGTGAGATGATCGATCTTCTTCAAC 467	
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AC	AAA29037;	
XX	12-SEP-2000 (first entry)	
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XX	B. napus flowering locus F (FLF) homologous cDNA 6.	
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XX	Flowering locus F; transcription factor; DNA binding domain; MADS box;	
KW	FLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.	
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OS	Brassica napus.	
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PR	22-JAN-1999;	99US-0116928P.	
XX	(CSIR ) COMMONWEALTH SCI & IND RES ORG.		
FA	(PERE) PEREZ P.		
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PI	Perez P, Burn JB, Peacock WJ, Dennis ES, Sheldon CC;		
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DR	WPI; 2000-451762/39.		
XX	P-PSDB; AAY96413.		
PT	New nucleic acid comprising a MADS box that encodes a transcription		
PT	factor for altering the flowering time or modifying the transcription or		
XX	floral phenotype of a plant such as wheat.		
PS	Claim 6; Page 88-89; 106pp; English.		
XX			
CC	AAA29032-41 are cDNA clones isolated from a Brassica napus cDNA library		
CC	using hybridisation to an FLF (flowering locus F) cDNA from Arabidopsis		
CC	thaliana. From both amino acid and nucleotide sequence data it was		
CC	concluded that the clones represent transcripts from 5 different genes.		
CC	The FLF gene encodes a transcription factor protein comprising a		
CC	distinctive conserved DNA binding domain (a MADS box). The DNA was		
CC	identified from a late-flowering mutant (elf), which arose during		
CC	transformation of the early-flowering ecotype C24 with a modified binary		
CC	vector pbin-delta-Ac. It was found that two T-DNAs segregate in the very		
CC	late flowering phenotype and that two expressed genes (A and B) were		
CC	closely linked to these T-DNAs. Gene B was re-designated as FLF. The FLF		
CC	gene is linked to the top of chromosome 5, 4 cm from RFLP marker 447. The		
CC	protein is capable of altering the flowering time of a plant. Over-		
CC	expression of the FLF gene can be used to delay flowering in a plant.		
CC	Alternatively, reduction of FLF gene expression, e.g. by antisense		
CC	constructs, can be used to induce early flowering. Methods of modifying		
CC	vegetative and/or floral phenotypes of a plant comprising increasing the		
CC	level of expression of a FLF gene to modify the production or activity of		
CC	a gibberellin in the plant are also claimed. The response of a plant to		
CC	vernalization can also be altered. Any dicotyledonous or monocotyledonous		
CC	plant species including horticultural plants, particularly those in the		
CC	cut-flower industry, vegetable, cereal and other crop plants are capable		
CC	of being controlled		
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Qy	205 TCGTCAAGTTTCTGTTCTCTGTGACGCATCCGTGCTCTTCTCGTCTCTCCGCTCCGG 264		
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Qy	325	ACAGCATGCTGATGATCTTAAAGCCTTGGATCATCAGTCAAAAGCTCTGAACCTATGGTTC	384
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Qy	385	ACACTATGAGCTACTTGAACCTTGGATAGCAAGCTTGTGGGATCAAAATGTCAAAAATGT	444
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Db	775	TAATGAGTAAATA	788

Search completed: May 22, 2006, 05:31:47  
Job time : 649 secs

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2006, 05:32:03 ; Search time 4482 Seconds  
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11765.268 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
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Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: gb\_est3:\*
- 3: gb\_est4:\*
- 4: gb\_est5:\*
- 5: gb\_est6:\*
- 6: gb\_hic:\*
- 7: gb\_est2:\*
- 8: gb\_est7:\*
- 9: gb\_est8:\*
- 10: gb\_est9:\*
- 11: gb\_ges1:\*
- 12: gb\_ges2:\*
- 13: gb\_ges3:\*
- 14: gb\_ges4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	590.8	62.7	899	10	DR749991 81-L02009
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4	507.4	53.8	769	8	CX267207 38RDBRM U
5	499.2	52.9	503	9	DR198395 1106125 C
6	487.4	51.7	701	8	CN730669 24RDBNH U
7	458.8	48.7	609	5	CD816564 EN20.00TA
8	417.8	44.3	606	8	CN737667 26RDBNT U
9	406.8	43.1	419	9	DR198394 73477 CER
10	372.4	39.5	655	9	DR262234 12822141
11	370.8	39.3	640	1	AU238414 12822141
12	362.8	38.5	673	4	CA781283 014D08AF
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21	299	31.7	492	10	DR350810
22	298.2	31.6	688	5	CD834584
23	295	31.3	727	8	CN736440
24	294.2	31.2	699	4	CB257827
25	290.8	30.8	919	10	DR749853
26	290.8	30.8	921	10	DR750371
27	281.2	29.8	492	9	DR262235
28	276.6	29.3	882	10	DR750372
29	269.8	28.6	474	9	DR262237
30	267.2	28.3	720	7	BE038655
31	263.2	27.9	520	9	DR210837
32	247.8	26.3	659	10	DR749854
33	246.2	26.1	690	3	BP796166
34	242.4	23.6	398	5	CD825381
35	218	23.1	469	1	AV553913
36	218	23.1	609	1	AU238299
37	218	23.1	662	10	DR369010
38	209.4	22.2	353	8	CX269606
39	209	22.2	642	11	BZ468975
40	207	22.0	352	9	DR262232
41	204.8	21.7	431	11	B96749
42	190	20.1	756	11	BZ069163
43	188.6	20.0	420	10	DR369009
44	184.6	19.6	434	1	AI994942
45	184.2	19.5	585	10	DR378623

ALIGNMENTS

RESULT 1  
DR749990

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

81-L020098-065-001-All-Sela MP1Z-ADIS-065d Arabidopsis thaliana  
cDNA clone 001-All, mRNA sequence.

DR749990 941 bp mRNA linear EST 19-JUL-2005  
DR749990.1 GI:71035330  
EST.

Arabidopsis thaliana (chale cress)  
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 941)  
Paz-Ares, J., Valencia, A., Costantino, P., Vittorioso, P., Davies, B.,  
Gilmartin, P., Giraudat, J., Parcy, F., Reindl, A., Sablowski, R.,  
Coupland, G., Martin, C., Angenot, G.C., Baumlein, H., Mock, H.P.,  
Carbonero, P., Colombo, L., Tonelli, C., Engstroem, P.,  
Droge-Laser, W., Gatz, C., Kavanagh, T., Kushnir, S., Zabeau, M.,  
Laux, T., Hordasewski, M., Ruberti, I., Ratcliff, P., Smeekens, S.,  
Somssich, I., Weishaar, B. and Traas, J.

REGIA, an EU project on functional genomics of transcription  
factors from Arabidopsis thaliana  
Comp. Funct. Genomics 3 (2), 102-108 (2002)

Contact:  
Paz-Ares, Costantino, Vittorioso, Davies, Gilmartin, Giraudat, Parcy, Sablowski, Coupland, Martin, Angenot, Baumlein, Carbonero, Colombo, Tonelli, Engstroem, Droge-Laser, Gatz, Kavanagh, Kushnir, Zabeau, Laux, Hordasewski, Ruberti, Smeekens, Somssich, Weishaar, Traas  
Bielefeld University, Institute for Genome Research  
Universitaetstrasse 25, D-33594 Bielefeld, Germany  
Email: bernd.weishaar@uni-bielefeld.de

AGI: AT5G10140; SeqAnalysis: full CDS correct; Translation: full  
good  
Data analysis performed in the frame of REGULATORS (Exploiting  
inter-species conservation in promoter sequences to identify  
regulators of reproductive development and physiological  
performance), a Trilateral CO-Operation in Plant Genomics between  
Spain (MCYT), France (GENOPLANTE) and Germany (GABI) coordinated by  
G. Coupland (coupland-ad-mpiz-koeln.mpg.de). Authors: Vincent  
Thareau (IBP-Orsay UMR8618 CNRS-UPS, thareau-ad-ibp.u-psud.fr) and  
Alain Lecharny (URGV-EVRY UMR INRA-CNRS-UEVE,



lecharny-ad-ibp.u-paud.fr).  
 Definition of the terms used to describe the quality of the clone:  
 The about 2250 sequences from the clone collection were sorted  
 according to clones and clustered. If more than one contig was  
 formed, the clone was designated 'Contamination'. The contigs and  
 singletons were blasted against CDS plus pseudogenes from the  
 TIGRv5 annotation, and the resulting AGI code is presented if more  
 than 90 percent identity was found. The sequences were also blasted  
 against all TIGRv5 introns, and matches longer than 50 bp with 95  
 percent identity are reported as 'intron found'. The remaining  
 terms for SeqAnalysis describe the outcome of the evaluation of the  
 CDS detected after pairwise alignment with CDS plus pseudogenes  
 from the TIGRv5 annotation file. The sequences or contigs for which  
 a full CDS with or without STOP codon was detected, a BLASTp  
 against all TIGRv5 protein sequences was performed. Full perfect:  
 100 percent identity; full good: better than 95 percent identity  
 over more than 95 percent of the sequence; partial good: better  
 than 95 percent identity over less than 95 percent of the sequence;  
 weak similarity: less than 95 percent identity over less than 95  
 percent of the sequence; no similarity: no hit from BLASTp. Note  
 that the collection contains a few clones for which sequencing was  
 not successful, which could have simple technical reasons.  
 Obviously, information about these clones is missing in the  
 submitted data.

Insert Length: 941 Std Error: 0.00

Seq primer: Seta TCGCGTTAACGCTAGCATGATGTC.

#### FEATURES source

Location/Qualifiers  
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/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/ecotype="Columbia"

/db\_xref="GABI:1452167"

/db\_xref="taxon:3702"

/clones="001-All"

/lab\_host="E. coli DH5alpha"

/clone\_lib="MP12-ADIS-065d"

/notes="Vector: pDONR201; In the context of the EU-funded project REGIA (OLG-CT11999-00876, coordinator Javier Paz-Ares), a set of transcription factor ORFs was generated. The ORFs were produced in a decentralized way in the labs of the participants. Most of the ORFs were generated by RT-PCR using cDNA from various A. thaliana tissues as a template. Initially, it was planned to use yeast recombination to move the ORFs from the cloning vectors into target constructs. For this reason, a number of the clones contain 'REGIA tags' (RG\_tag):

5pr-AATTCAGTCCACC-3pr; RG\_tag2:

5pr-CATGGCAATCCGGGATC-3pr). During the lifetime of the project, the GATEWAY system became available and finally all ORFs were transferred into GATEWAY vectors. At the end of the REGIA project, the clones were collected as plasmid DNA. For end-sequencing at the DNA core facility of the MPI of Plant Breeding Research (ADIS; head: Bernd Weisshaar), the plasmids were re-transformed into DH5alpha, arrayed into 96-well plates and new plasmid DNA was prepared. Re-transformation proved to be difficult because a number of clones displayed poor growth. Data submission has been handled by GabiFD (<http://gabi.rzpd.de>)."

#### ORIGIN

Query Match 62.9%; Score 593.4; DB 10; Length 941;  
 Best Local Similarity 99.0%; Pred. No. 5.6e-142;  
 Matches 597; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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 Db 83 CGGGTATTCACCATCGGAGAGAAAAAATAGAAATCAAGCGAATTCGAGACAAAGTAGC 142  
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 Qy 158 CGACAGTACCTTCTCCAAACGTCGACCGGTCTCATCGAGAAAGCTGTCAGCTTTCT 217  
 |||||  
 Db 143 CGAAGATGACCTTCTCCAAACGTCGACCGGTCTCATCGAGAAAGCTGTCAGCTTTCT 202  
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Qy 218 GTTCTCTGTGACGATCCGTCGCTCTTCTCGTGTCTCCGCTCCGCGCAAGCTCTACAGC 277  
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 Db 203 GTTCTCTGTGACGATCCGTCGCTCTTCTCGTGTCTCCGCTCCGCGCAAGCTCTACAGC 262  
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 Qy 278 TTCTCTCCGCGGATAAACCTGGTCAAGATCTCTTGATCGATATGGGAAACAGCATGCTGAT 337  
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 Db 263 TTCTCTCCGCGGATAAACCTGGTCAAGATCTCTTGATCGATATGGGAAACAGCATGCTGAT 322  
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 Qy 338 GATCTTAAGCCCTTGGATCATAGTCAAAAGCTCTGAATATGTTTACACTATGAGCTA 397  
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 Db 323 GATCTTAAGCCCTTGGATCATAGTCAAAAGCTCTGAATATGTTTACACTATGAGCTA 382  
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 Qy 398 CTTGAACCTTGTGATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCT 457  
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 Db 383 CTTGAACCTTGTGATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCT 442  
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 Db 443 CTTGTTTCAACTGGAGGAACACCTTTGAGACTGCCCTCTCCGTGACTAGAGCCAAAGAGACC 502  
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 Qy 698 TAG 700  
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 Db 683 TAG 685

RESULT 2  
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 cDNA clone 001-All, mRNA sequence.  
 DR749991  
 ACCESSION  
 DR749991.1 GI:71035331  
 VERSION  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.  
 1 (bases 1 to 899)  
 REFERENCE  
 AUTHORS  
 Paz-Ares, J., Valencia, A., Costantino, P., Vittorioso, P., Davies, B.,  
 Gilmarin, P., Giraudat, J., Parcy, F., Reindl, A., Sablowski, R.,  
 Coupland, G., Martin, C., Angenent, G. C., Baumeister, H., Mock, H. P.,  
 Carbonero, P., Colombo, L., Tonelli, C., Engstrom, P.,  
 Droge-Laser, W., Gatz, C., Kavanagh, T., Kushnir, S., Zabeau, M.,  
 Laux, T., Hordworth, M., Ruberti, I., Ratcliff, P., Smeekens, S.,  
 Somsich, I., Weisshaar, B. and Traas, J.  
 REGIA, an EU project on functional genomics of transcription  
 factors from Arabidopsis thaliana  
 Comp. Funct. Genomics 3 (2), 102-108 (2002)  
 TITLE  
 JOURNAL  
 COMMENT  
 Contact:  
 Paz-Ares, Costantino, Vittorioso, Davies, Gilmarin, Giraudat, Parcy, Sabl  
 owski, Coupland, Martin, Angenent, Baumeister, Carbonero, Colombo, Tonelli,  
 Engstrom, Droge-Laser, Gatz, Kavanagh, Kushnir, Zabeau, Laux, Hordworth  
 Ruberti, Smeekens, Somsich, Weisshaar, Traas  
 Bielefeld University, Institute for Genome Research  
 Universitaetsstrasse 25, D-33594 Bielefeld, Germany  
 Email: bernd.weisshaar@uni-bielefeld.de  
 AGI: AT5G10140; SeqAnalysis: full CDS correct; Translation: full  
 good  
 Data analysis performed in the frame of REGULATORS (Exploiting  
 inter-species conservation in promoter sequences to identify



/db\_xref="taxon:3702"  
/clone="39347"  
/tissue type="Mixed floral buds, roots (9:1)"  
/clone\_lib="CERES-148"

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Query Match 61.3%; Score 578.2; DB 10; Length 595;  
Best Local Similarity 99.2%; Pred. No. 4.3e-138;  
Matches 592; Conservative 0; Mismatches 3; Indels 2; Gaps 1;  
QY 158 CGCAAGTCACCTTCTCCAAAGTCGCAAGCTCTCATCGAAGAGCTCGTCAGCTTTCT 217  
Db 1 CGCAAGTCACCTTCTCCAAAGTCGCAAGCTCTCATCGAAGAGCTCGTCAGCTTTCT 60  
QY 218 GTTCTCTGTGACGATCCGTCGCTCTTCTGTGCTCTCCGCTCCGCGCAAGCTCTACAGC 277  
Db 61 GTTCTCTGTGACGATCCGTCGCTCTTCTGTGCTCTC--CCTCCGCAAGCTCTACAGC 118  
QY 278 TTCTCTCCGCGGATAACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGAT 337  
Db 119 TTCTCTCCGCGGATAACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGAT 178  
QY 338 GATCTTAAAGCCTTGGATCATCAGTCAAAAGCTCTGAACATATGGTTTCACTATGAGCTA 397  
Db 179 GATCTTAAAGCCTTGGATCATCAGTCAAAAGCTCTGAACATATGGTTTCACTATGAGCTA 238  
QY 398 CTTGAACTCTGGATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCT 457  
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QY 458 CTTGTTCAACTGGAGGAACACCTTGAGACTGCCCTCTCCGTGACTAGAGCCAAAGAGACC 517  
Db 299 CTTGTTCAACTGGAGGAACACCTTGAGACTGCCCTCTCCGTGACTAGAGCCAAAGAGACC 358  
QY 518 GAATCATGTTGAAGCTTGTGAGATCTTAAAGAAAGAGAAAATGCTGAAAGAGAG 577  
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QY 578 AACAGGTTTGTGCTAGCAGATGGAGAAATATCATCATGTGGGAGCAGAGCTGAGATG 637  
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Db 479 GAGATGTCACCTCTCGCAAAATCTCCGCAATCTTCCGCTGACTCTCCCACTACTTAAT 538  
QY 698 TAGCCACCTTAATCCGCGGTTGAAATCAAAATCAGATATATATTAAGA 754  
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## RESULT 4

CX267207  
LOCUS 769 bp mRNA linear EST 22-DEC-2005  
DEFINITION 38RDBRM UP\_019\_C08\_02APR2004\_060 Brassica rapa 38RDBRM Brassica  
rapa cDNA 5', mRNA sequence.

CX267207  
ACCESSION CX267207.1 GI:83818984

KEYWORDS EST.

SOURCE Brassica rapa (Brassica campestris)

## ORGANISM

Brassica rapa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1. (bases 1 to 769)

Xiang,D., Venglat,P., Keller,G., Selvaraj,G. and Datla,R.

Gene Expression Patterns during Brassica Zygotic Embryogenesis

Unpublished (2004)

TITLE

JOURNAL

COMMENT

Contact: Raju Datla

Molecular and Developmental Genetics

National Research Council of Canada

Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,

Saskatchewan, S7N 0W9, Canada

Tel: 306 975 5267  
Fax: 306 975 4839  
Email: Raju.Datla@nrc-cnrc.gc.ca  
High quality sequence stop: 769.

## FEATURES

## Source

1. 769  
/organism="Brassica rapa"  
/mol\_type="mRNA"  
/db\_xref="taxon:3711"  
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/notes="Vector: pDNR-LIB CREATOR; Site 1: Sfi IA; Site 2:  
Sfi IB; Brassica rapa 38RDBRM. Sequences have been trimmed  
to remove vector and low quality regions using LUCY  
sequence cleanup software (www.tigr.org)."

## ORIGIN

Query Match 53.8%; Score 507.4; DB 8; Length 769;  
Best Local Similarity 83.5%; Pred. No. 9.1e-120;  
Matches 624; Conservative 0; Mismatches 116; Indels 7; Gaps 4;  
QY 5 AAAGGAAAAAATAAGAAAGAAAAAGC--TTAGTATCTCCGCGCAGCTTGAACCCA 63  
Db 23 AAAGGAAAAAATAAGAAAGAAAAAGCATAAAACGCTTTAGTATCTCCGCGCAGCTTGA 81  
QY 64 AACCTCAGGATCAAAATTAGGGCAAAAGCCCTCTCGAG--AGAAGCCATGGGAAGAAA 121  
Db 82 AACCTCTGGATCAAAATTAGGGCAAGAGACCCTTGGAGACAGAAACCATGGGAAGAAA 141  
QY 122 AAACCTAGAAATCAAGCGAATTGAGAACAAAAAGTAGCCCAAGTCACTTCTCCAAACGT 181  
Db 142 AAACCTAGAAATCAAGCGAATTGAGAACAAAAAGTAGCCCAAGTCACTTCTCCAAACGA 201  
QY 182 CGCAACGCTCTCATCGAAGAAAGCTCGTCACTTTCTGTCTCTGTGACGATCCGTCGCT 241  
Db 202 CGCAGCGCTCTCATTTGAGAAAGCTCGTCACTTTCTGTCTCTGTGACGATCCGTCGCG 261  
QY 242 CTTCTCGTCTCGCTCCGCTCCGCGCAGCTCTACAGCTTCTCCTCCGCGCAGTAACCTGGTC 301  
Db 262 CTTCTCGTCTCTCTCTCTCCGCGCAGCTCTACAGCTTCTCCTCCGCGGTGATAACCTGGTC 321  
QY 302 AAGATCTCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCCTTGGATCATCAG 361  
Db 322 AGGATCTCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCCTGATCTTCAG 381  
QY 362 TCAAAAGCTCTCAACTATGTTTCACTATGAGTACTTGAACCTTGTGATAGCAAGCTT 421  
Db 382 TCANAAGCTCTGAGCTATGGTTTCACTATGAGTTACTTTGAACTTTGTGATAGCAAGCTT 441  
QY 422 GTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTTTGTTCAACTGGGGAACACCTT 481  
Db 442 GTGGATCAAAATGTGAGTATGAGCTGGGACACCTCTGTCAGCTGGAGGTGTCTT 501  
QY 482 GAGACTGCCCTCTCCGTGACTAGAGCCAAAGAACCGAACTCATGTTGAAGCTTGTGAG 541  
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QY 542 AATCTTAAAGAAAGAGAGAAATGCTGAAAGAGAACAGAGTTTGTGCTAGCCAGATG 601  
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QY 602 GAGAAATATCATATGTCGGAGCAGAGCTGAGATGAGATGTCACCTGCTCGACAAATC 661  
Db 622 GAGAAAGAAATCTTTCCGGAGCCGAGCTGATATATGAGATGTACCTGCTCGACAAATC 681  
QY 662 TCCGA---CAATCTTCCGCTGACTCTCCCACTACTTAATTTAGCCACCTTAAATTCGCGGT 718  
Db 682 TCCGACATCAATCTTCCGCTAATCTCTCCCACTGCTTAATTTAGCCACCTTGTAGACGGGCT 741  
QY 719 TGAATCAAAATCCAAACATATATAA 745  
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Qy	483	AGACTGCCCTCTCCGTGACTAGAGCCCAAGAGACCGAATCACTGTTGAGCTTGTGAGA	542	Qy	253	CTCCGCTCCGCAAGCTCTACAGCTTCTCCTCCGGGATAACCTGGTCAAGATCCTTGA	312	
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Db	484	ACCTTAAAGAAAAGGAGAAAGTGTCTGGAAGAGAGAACCATGTTTGGCTAGCCAGATGG	543	Db	241	TCGATACGGAAAGCAACATGGTGATGATCTTTAAAGCCTTGGATCGTCAGTCAAAAGCTTT	300	
Qy	603	AGAAATCATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACTCTCTGACAAA---	659	Qy	373	GAACTATGTTTCACTATGAGCTACTTTGAACTTGTGGATAGCAAGCTTGTGGGATCAAA	432	
Db	544	AGAAGAGTAATCTTGTGCGAGCGAAGCTGATAATATGAGAGTGTCACTTGGAACAAATC	603	Db	301	GGACTCTGCTTTCACCATGAGCTGTGGAACCTTGTGGAAAGCAAGCTTGGAGGAATCAAA	360	
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Db	604	TCCGACATCAATCTTCTGGTAACGCTCCCACTGCTTAATATGTTACCGTTAATTCGGGAA	663	Db	361	TGTCGATAATGTAAGTGTGGGTTCCCTGGTTCAGCTGGAGGAAACACCTTGGAAACGCCCT	420	
Qy	719	TGAAATCAAAAATCCAAAACATATATATTAATTAAGAA 755		Qy	493	CTCCGTGACTAGAGCCAAAGAACCGAACTCATGTTGAAGCTTGTGAGAACTCTTAAAGA	552	
Db	664	TAAATAAAATCCCAACATATTAATTAACAAACAA 700		Db	421	CTCCGTAAACAGAGCTAGGAAGACAGAACTAATGTTGAAGCTTGTGGAACCTTAAAGA	480	
RESULT 7				Qy	553	AAAGGAGAAAATGCTGAAAGAGAGAACCAAGGTTTGGCTAGCCAGATGGAGAAATATCA	612	
CD816564				Db	481	AAAGGAGAAAGTTGCTGGAGAGGAGAACCATGTTTGGCTAGCCAGATGGAGAGAGTAA	540	
DEFINITION	BN20_001A12F010914 BN20 Brassica napus cDNA clone BN20001A12, mRNA			Qy	613	TCATGTGGGAGCAGAGCTGAGATGGAGATGTCACCTGCTGGACAAATCTCCGACA	668	
ACCESSION	CD816564			Db	541	TCTTGTGCGAGCCGAAAGCTGATAATATGAGAGGTGTACCTGGACAAATCTCCGACA	596	
VERSION	CD816564.1 GI:32498504			RESULT 8				
KEYWORDS	EST.			CN737667				
SOURCE	Brassica napus (rape)			LOCUS				
ORGANISM	Brassica napus			DEFINITION	CN737667	606 bp mRNA linear EST 14-MAY-2005		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.			ACCESSION	CN737667	napus cDNA 5', mRNA sequence.		
AUTHORS	Genoplante.			VERSION	CN737667.1	GI:65295486		
JOURNAL	Genoplante, a major partnership french program in plant genomics			KEYWORDS	EST.			
COMMENT	Contact: Genoplante Unpublished (2003) Genoplante 93, rue Henri Rochefort 91025 EVRY CEDEX France Tel: 33 1 69 47 54 00 Fax: 33 1 69 47 54 10 This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' ( <a href="http://www.genoplante.com">http://www.genoplante.com</a> ) and <a href="http://genoplante-info.infobiogen.fr">http://genoplante-info.infobiogen.fr</a> .			SOURCE	Brassica napus (rape)			
FEATURES	Location/Qualifiers			ORGANISM	Brassica napus			
source	1..609 /organism="Brassica napus" /mol_type="mRNA" /cultivar="Jet Neuf" /db_xref="taxon:3708" /clone="BN20001A12" /tissue_type="seed" /clone_lib="BN20"			REFERENCE	Xiang,D., Venglat,P., Keller,G., Selvaraj,G. and Datla,R. Gene Expression Patterns during Brassica Zygotic Embryogenesis Unpublished (2004) Contact: Raju Datla Molecular and Developmental Genetics National Research Council of Canada Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, Saskatchewan, S7N 0W9, Canada Tel: 306 975 5267 Fax: 306 975 4839 Email: Raju.Datla@nrc-cnrc.gc.ca High quality sequence stop: 606. Location/Qualifiers 1..606 /organism="Brassica napus" /mol_type="mRNA" /db_xref="taxon:3708" /clone_lib="Brassica napus 26RDBNT" /note="Vector: pDNR-LIB_CREATOR; Site_1: Sfi 1A; Site_2: Sfi 1B; Zygotic embryos at torpedo stage from Brassica napus seeds were used for the isolation of PolyA RNA and in the construction of the cDNA library. Sequences have been trimmed to remove vector and low quality regions using LUCY sequence cleanup software ( <a href="http://www.tigr.org">www.tigr.org</a> )."			
ORIGIN				FEATURES				
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Qy	75	CAAAATTAGGGCAAAAGCCCTCTCGAG--AGAGCCATGGGAAGAAAAAACTAGAAT	132					
Db	1	CAAAATTAGGGCGAAAGCCCGTTGGAGACAGAAAGCATGGGAGAAAGAACTTGAAT	60					
Qy	133	CAAGCGAATTGAGAACAAAGTAGCCGACAGTCACTTCTCCAAAGTCGCAACGGTCT	192					
Db	61	CAAGCGATTGAGAACAAAGTAGCCGACAGTCACTTCTCCAAAGTCGCAACGGTCT	120					
Qy	193	CATCGAGAAAGCTCGTCAGCTTTCTGTTCTCTGTGACGCATCCGTCGCTCTTCTCGTCT	252					
				Query Match	44.3%; Score 417.8; DB 8; Length 606;			

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Best Local Similarity 86.7%; Pred. No. 1.2e-96;
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Qy 3 AGAAAGGAAAAAATAAGAGAAAAACG-TPAGTATCTCCGGCGACTTGAACC 61
Db 37 AAAAAAGGAAAAAATAAGAGAAAAACGCTTTAGTATCTCCGGCGACTTGAACC 96

Qy 62 CAACCTGAGGATCAAAATAGGACCAAAAGCCCTCTCGAG--AGAGCCATGGAGAA 119
Db 97 GAACCCCT-GGATCAAAATAGGACCAAAAGCCCTCTCGAGACAGAAACCAATGGAGAA 155

Qy 120 AAAAAGTAGAAATCAAGCGAATTCAGACCAAAAGTAGCCCAAGTACACCTTCTCCAAAC 179
Db 156 AAAAAGTAGAAATCAAGCGAATTCAGACCAAAAGTAGCCCAAGTACACCTTCTCCAAAC 215

Qy 180 GTCCGAACGGTCTCATTCGAGAAAGCTCGTCAGCTTTCTGTTCTCTGTGACGCATCCGTGG 239
Db 216 GACGACGGTCTCATTCGAGAAAGCTCGTCAGCTTTCTGTTCTCTGCGATCATCCGTGG 275

Qy 240 CTCTTCTCGTCTCTCCGCTCCGGCAAGCTCTACAGCTTCTCTCCGGCGATTAACCTGG 299
Db 276 CGCTTCTCGTCTCTCCGCTCCGGCAAGCTCTACAGCTTCTCCGGCGATTAACCTGG 335

Qy 300 TCAAGATCCTTTGATCGGATATGGGAAACAGCATGCTGATGATCTTAAAGCCCTTGCATCATC 359
Db 336 TCAGGATCCTTTGATCGGATATGGGAAACAGCATGCTGATGATCTTAAAGCCCTTGCATCATC 395

Qy 360 AGTCAAAAGCTCTGAACTATGTTTACACTATGAGTACTTGAAGCTTGTGGATAGCAAGC 419
Db 396 AGTCAAAAGCTCTGAGCTATGTTTACACTATGAGTACTTGAAGCTTGTGGATAGCAAGC 455

Qy 420 TTGTGGGATCAAAATGTCGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 479
Db 456 TTGTGGGATCAAAATGTCGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 515

Qy 480 TTGAGATGCGCTCTCCGCTGACTAGAGCAAGAGAGCGAAGTCTTGTGTTCAACTGAGGAAAC 539
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Qy 540 AGAATCTTAAAGAAAAAGGAGAAAAATCTGAA 570
Db 576 ATAGCTTAAAGAAAAAGGAGAAAGCTGCTGAA 606

RESULT 9
DR198394
LOCUS 73477 CERES-148 Arabidopsis thaliana cDNA clone 39347 5', mRNA
DEFINITION sequence.
ACCESSION DR198394.1 GI:85877436
VERSION DR198394.1
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 419)
Alexandrov,N.N., Troukhan,M.E., Brover,V.V., Tatarinova,T.,
Lu,Y.-P., Flavell,R.B. and Feldmann,K.A.
Features of Arabidopsis genes and genome discovered using
full-length cDNAs
Plant Mol. Biol. 60 (1), 71-87 (2006)
Contact: Alexandrov NN
Ceres, Inc
1535 Rancho Conejo Blvd., Thousand Oaks, CA 91320, USA
Tel: (805) 376-6539
Fax: (805) 498-1002
Email: nalexandrov@ceres-inc.com.
Location/Qualifiers
1. .419
/organism="Arabidopsis thaliana"
/mol_type="mRNA"

FEATURES
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Matches 416; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy 2 GAGAAAGGAAAAAATAAGAGAAAAACGCTTAGTATCTCCGGCGACTTGAACC 61
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Qy 62 CAACCTGAGGATCAAAATAGGACCAAAAGCCCTCTCGAGAGAAAGCCATGGGAGAAAAA 121
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Db 180 CGCAACGGTCTCATTCGAGAAAGCTCGTCAGCTTCTCTCTGTGACGCATCCGTGGCT 239

Qy 242 CTCTCTCGTCTCTCCGCTCCGGCAAGCTCTACAGCTTCTCTCCGGCGATAACCTGGTC 301
Db 240 CTCTCTCGTCTCTCCGCTCCGGCAAGCTCTACAGCTTCTCTCCGGCGATAACCTGGTC 299

Qy 302 AAGATCCTTCGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCCTTGGATCATCAG 361
Db 300 AAGATCCTTCGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCCTTGGATCATCAG 359

Qy 362 TCAAGAGCTCTGAACTATGTTTACACTATGAGTACTTGAAGCTTGTGGATAGCAAGCTT 421
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LOCUS 12822141 CERES-AN65 Arabidopsis thaliana cDNA clone 1357903 5',
DEFINITION mRNA sequence.
ACCESSION DR262234.1 GI:85941255
VERSION DR262234.1
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 655)
Alexandrov,N.N., Troukhan,M.E., Brover,V.V., Tatarinova,T.,
Lu,Y.-P., Flavell,R.B. and Feldmann,K.A.
Features of Arabidopsis genes and genome discovered using
full-length cDNAs
Plant Mol. Biol. 60 (1), 71-87 (2006)
Contact: Alexandrov NN
Ceres, Inc
1535 Rancho Conejo Blvd., Thousand Oaks, CA 91320, USA
Tel: (805) 376-6539
Fax: (805) 498-1002
Email: nalexandrov@ceres-inc.com.
Location/Qualifiers
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Best Local Similarity 75.9%; Pred. No. 6.8e-85;									
Matches 460; Conservative 0; Mismatches 146; Indels 0; Gaps 0;									
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DB	1	GAAGCCATGGGAAGAAAAAATTCGAGATCAGCGAATTCGAAACAAAAGCATGACAA	60						
QY	164	GTCACTTTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTTCTC	223						
DB	61	GTCACTTTCTCCAAACGAGCAATGGTCTCATCGAACAAGCTCGCAACACTTTGATTTCTC	120						
QY	224	TGTGAGCATCCCTCGCTCTTCTGTCGTCCTCGCTCCGGCAAGCTCTACAGCTTCTCC	283						
DB	121	TGTGAATCTCTCGCTCGCTGTTGTCGTCGTCCTCGCTCCGGAAACCTCTATGACTCTTC	180						
QY	284	TCCGGCGATAAACCCTGGTCAAGATCTTGTATCGATATGCGAAACAGCATGCTGATGATCTT	343						
DB	181	TCCGGTGAAGACATTTCCAGATCATTTCCAAAGATCATTTGATCGTTATGAAATACAACTGATGAAC	240						
QY	344	AAAGCCTTTGGATCATCAGTCAAAAGCTCTGAACTATGTTTCACTATGAGCTTACTTGAA	403						
DB	241	AGAGCCTTAGATCTTGAGAAAAAATTCAGATTATCTTCCACACAAGGAGTTACTAGAA	300						
QY	404	CTTTGGATAGCAAGCTTTGTTGGGATCAAATGTCAAAAATGTGAGTATCGATGCTTTGTT	463						
DB	301	ACAGTCCAAAGCAAGCTTTGAAGAACAAATGTCGATAATGTAAGTGTAGATTCTCTAAAT	360						
QY	464	CAACTGGAGGAACACCTTTGAGACTCCCTCTCCGTGACTAGAGCCNAGAACCCGAACTC	523						
DB	361	TCTCTGGAGGAACAACTTTGAGACTCTCTGTCGTCGTCCTCGCTCCGGAAACCTCTATGACTCTTC	420						
QY	524	ATGTTGAAGCTTTGTGAGAAATCTTAAAGAAAGGAGAAATCTGAAAGAAAGAACACCA	583						
DB	421	ATGATGGAGTATATCGAGTCCCTTAAAGAAAGGAGAAATTCCTGAGAGAGAACCA	480						
QY	584	GTTTTGGCTAGCCAGATGGAGAAATATCATATGTGGGAGCAGAAAGCTGAGATGGAGATG	643						
DB	481	GTTCCTGGCTAGCCAGATGGAGAAAGATACGTTGCTGGCAACAGATGATGAGAGAGAA	540						
QY	644	TCACCTGCTGGNCAATCTCCGACAACTCTCCGGTGAATCTCCGCTGACTCTCCCACTACTT	703						
DB	541	TTTCCGGGAAGTAGCTCCGGCAACAAATATACGGGAGACTCTCCCGCTGCTCAATTAGCCA	600						
QY	704	CCTTAA	709						
DB	601	CCATCA	606						
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LOCUS AU238414 RAPL17 Arabidopsis thaliana cDNA clone RAPL17-22-J12 5',									
DEFINITION mRNA sequence.									
ACCESSION AU238414									
VERSION AU238414.1 GI:19877583									
SOURCE EST.									
ORGANISM Arabidopsis thaliana (thale cress)									
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;									
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;									
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.									
1 (bases 1 to 640)									
Akiyama, K., Enju, A., Oono, Y., Sakurai, T., Carninci, P., Kawai, J.,									
Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A.,									
Murmatsu, M., Hayashizaki, Y. and Shinozaki, K.									
Large scale analysis of Arabidopsis full-length cDNA									
Unpublished (2002)									
Contact: Motoaki Seki									
TITLE									
JOURNAL									
COMMENT									

Plant Functional Genomics Research Group									
RIKEN Genomic Sciences Center									
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan									
Tel: 81-298-36-4359									
Fax: 81-298-36-9060									
Email: mseki@tc.riken.go.jp									
An Arabidopsis full-length cDNA library was constructed essentially									
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI									
and XhoI was ligated to modified lambda PUC-1 vector (Carninci et									
al., submitted for publication) digested with BamHI and SalI. This									
clone is in a modified pBluescript vector. Please visit our web									
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further									
details.									
FEATURES									
source									
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/note="Site 1: BamHI; Site 2: SalI; Subtraction library.									
The sequence was obtained from samples subjected to									
dehydration-treated (1, 2, 5, 10 and 24 hr) and									
rehydration-treated (1, 2, 5, 10, and 24 hr after									
dehydration treatment)"									
ORIGIN									
Query Match 39.3%; Score 370.8; DB 1; Length 640;									
Best Local Similarity 75.7%; Pred. No. 1.7e-84;									
Matches 459; Conservative 0; Mismatches 147; Indels 0; Gaps 0;									
QY	104	GAAGCCATGGGAAGAAAAAATAGAAATCAAGCGAATTCAGAAACAAAAGTAGCCGACAA	163						
DB	1	GAGGCCATGGGAAGAAAAAATTCGAGATCAAGCGAATTCGAAACAAAAGCATGACAA	60						
QY	164	GTCACTTTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTTCTC	223						
DB	61	GTCACTTTCTCCAAACGAGCAATGGTCTCATCGAACAAGCTCGAACAATTCGATTTCTC	120						
QY	224	TGTGAGCATCCGTGCTCTTCTGTCGTCCTCGCTCCGGCAAGCTCTACAGCTTTCTCC	283						
DB	121	TGTGAATCTCTCGTCTGTCGTCGTCCTCGCTCCGGAAACCTCTATGACTCTTC	180						
QY	284	TCCGGCGATAAACCCTGGTCAAGATCTTGTATCGATATGCGAAACAGCATGCTGATGATCTT	343						
DB	181	TCCGGTGAAGACATTTCCAGATCATTTCCAAAGATCATTTGATCGTTATGAAATACAACTGATGAAC	240						
QY	344	AAAGCCTTTGGATCATCAGTCAAAAGCTCTGAACTATGTTTCACTATGAGCTTACTTGAA	403						
DB	241	AGAGCCTTAGATCTTGAGAAAAAATTCAGATTATCTTCCACACAAGGAGTTACTAGAA	300						
QY	404	CTTTGGATAGCAAGCTTTGTTGGGATCAAATGTCAAAAATGTGAGTATCGATGCTTTGTT	463						
DB	301	ACAGTCCAAAGCAAGCTTTGAAGAACAAATGTCGATAATGTAAGTGTAGATTCTCTAAAT	360						
QY	464	CAACTGGAGGAACACCTTTGAGACTCCCTCTCCGTGACTAGAGCCNAGAACCCGAACTC	523						
DB	361	TCTCTGGAGGAACAACTTTGAGACTCTCTGTCGTCGTCCTCGCTCCGGAAACCTCTATGACTCTTC	420						
QY	524	ATGTTGAAGCTTTGTGAGAAATCTTAAAGAAAGGAGAAATCTGAAAGAAAGAACACCA	583						
DB	421	ATGATGGAGTATATCGAGTCCCTTAAAGAAAGGAGAAATTCCTGAGAGAGAACCA	480						
QY	584	GTTTTGGCTAGCCAGATGGAGAAATATCATATGTGGGAGCAGAAAGCTGAGATGGAGATG	643						
DB	481	GTTCCTGGCTAGCCAGATGGAGAAAGATACGTTGCTGGCAACAGATGATGAGAGAGAA	540						
QY	644	TCACCTGCTGGNCAATCTCCGACAACTCTCCGGTGAATCTCCGCTGACTCTCCCACTACTT	703						
DB	541	TTTCCGGGAAGTAGCTCCGGCAACAAATATACGGGAGACTCTCCCGCTGCTCAATTAGCCA	600						
QY	704	CCTTAA	709						



[illegible]

against all TIGRv5 protein sequences was performed. Full perfect: 100 percent identity; full good: better than 95 percent identity over more than 95 percent of the sequence; partial good: better than 95 percent identity over less than 95 percent of the sequence; weak similarity: less than 95 percent identity over less than 95 percent of the sequence; no similarity: no hit from BLASTp. Note that the collection contains a few clones for which sequencing was not successful, which could have simple technical reasons. Obviously, information about these clones is missing in the submitted data.

Insert Length: 936 Std Error: 0.00

Seq primer: Seta TCGGTTAACTGCTAGCATGGATCTC.

#### FEATURES

##### source

Location/Qualifiers  
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/mol\_type="mRNA"  
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/clone="001-B01"  
/lab\_host="E. coli DH5alpha"  
/clone\_lib="MPI2-ADIS-065d"  
/note="Vector: pDONR201; In the context of the EU-funded Project REGIA (QLG-CT11999-00876, coordinator Javier Paz-Ares), a set of transcription factor ORFs was generated. The ORFs were produced in a decentralized way in the labs of the participants. Most of the ORFs were generated by RT-PCR using cDNA from various A. thaliana tissues as a template. Initially, it was planned to use yeast recombination to move the ORFs from the cloning vectors into target constructs. For this reason, a number of the clones contain 'REGIA tags' (RG tag1: 5'-AATTCGATCCATCCACC-3pr; RG tag2: 5'-CATGCGCAATCCCGGATC-3pr). During the lifetime of the project, the GATEWAY system became available and finally all ORFs were transferred into GATEWAY vectors. At the end of the REGIA project, the clones were collected as plasmid DNA. For end-sequencing at the DNA core facility of the MPI of Plant Breeding Research (ADIS; head: Bernd Weishaar), the plasmids were re-transformed into DH5alpha, arrayed into 96-well plates and new plasmid DNA was prepared. Re-transformation proved to be difficult because a number of clones displayed poor growth. Data submission has been handled by GabipD (<http://gabi.rzpd.de>)."

##### ORIGIN

Query Match 36.6%; Score 345.2; DB 10; Length 936;  
Best Local Similarity 73.6%; Pred. No. 7.9e-78;  
Matches 440; Conservative 0; Mismatches 158; Indels 0; Gaps 0;  
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DB 84 GGAATTCATGGGTAGAAAAAAGTCGATCAAGCGAATTCAGACAAAGTACCGAC 143  
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DB 144 AAGTACCTTTCCAAACGCGCAATGGTCTCATCGAGAAAGTCGCAACCTTCAATTC 203  
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QY 282 CTTCCGGCGTAACCTGGTCAGAGTCCTTGATCGATATGGGAAACAGCATGCTGATGTC 341  
DB 264 CTTCCGGTGACAAATGTCAAAGATCATTTGATCGTTTACGAAATATCATCATGCTGATGAC 323  
QY 342 TTAAGACCTTGGATCATCAGTCAAAAGCTCTGAACTATGTTTCACACTATGAGTACTTG 401  
DB 324 TTGAAGCCTTAGATCTTTCGAGAAAAAATCGGAATATCTGCCATCTCAAGAGTTACTAG 383  
QY 402 AACTTGTGATAGCAAGCTTTGGGATCAATATGTCAAAAAATGTAGATTCGATGCTCTTG 461

Db 384 AAATAGTCCAAAGCAAGCTTGAAGAATCAAAATGTCGATATGCAAGTGTGGACTTTAA 443  
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Db 564 AGACTTTGGCTAGCCAGGTGGGAGAGACAGCGTTTCTGTTATAGAAAGGTGACAGAGAA 623  
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Db 624 TGTCTAGGAAAAATGGCTCCGGCAACAAAGATACGGGAGAGACTCTTCGCTGCTCAAGTA 681

##### RESULT 14

##### DR751519/c

##### LOCUS

##### DEFINITION

##### ACCESSION

##### VERSION

##### KEYWORDS

##### SOURCE

##### ORGANISM

##### REFERENCE

##### AUTHORS

##### TITLE

##### JOURNAL

##### COMMENT

DR751519 896 bp mRNA linear EST 19-JUL-2005  
02-L020099-065-001-B01-SeLB MP12-ADIS-065d Arabidopsis thaliana  
cDNA clone 001-B01, mRNA sequence.  
DR751519  
DR751519.1 GI:71036859  
EST  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 896)  
Paz-Ares, J., Valencia, A., Costantino, P., Vittorioso, P., Davies, B.,  
Gilmartin, P., Giraudat, J., Parcy, F., Reindl, A., Sablowski, R.,  
Coupland, G., Martin, C., Angenent, G. C., Baumeister, H., Mock, H. P.,  
Carbonero, P., Colombo, L., Tonelli, C., Engstrom, P.,  
Droge-Laser, W., Gatz, C., Kavanagh, T., Kushnir, S., Zabeau, M.,  
Laux, T., Hordworth, M., Ruberti, I., Ratcliff, F., Smeekens, S.,  
Somsich, I., Weishaar, B. and Traas, J.  
REGIA, an EU project on functional genomics of transcription  
factors from Arabidopsis thaliana  
Comp. Funct. Genomics 3 (2), 102-108 (2002)  
Contact:

Paz-Ares, Costantino, Vittorioso, Davies, Gilmartin, Giraudat, Parcy, Sablowski, Coupland, Martin, Angenent, Baumeister, Carbonero, Colombo, Tonelli, Engstrom, Droge-Laser, Gatz, Kavanagh, Kushnir, Zabeau, Laux, Hordworth, Ruberti, Smeekens, Somsich, Weishaar, Traas  
Bielefeld University, Institute for Genome Research  
Universitaetstrasse 25, D-33594 Bielefeld, Germany  
Email: bernd.weishaar@uni-bielefeld.de  
AGI: AT5G65050; SeqAnalysis: structure problem; Translation: no full cds detected  
Data analysis performed in the frame of REGULATORS (Exploiting inter-species conservation in promoter sequences to identify regulators of reproductive development and physiological performance), a Trilateral Co-Operation in Plant Genomics between Spain (MCYT), France (GENOPLANTE) and Germany (GABI) coordinated by G. Coupland (coupland-ad-mpiz-koeln.mpg.de). Authors: Vincent Thareau (thareau-umr9618 CNRS-UPS, thareau-ad-ibp.u-psud.fr) and Alain Lecharny (URGV-Evry UMR INRA-CNRS-UEVE, lecharny-ad-ibp.u-psud.fr).  
Definition of the terms used to describe the quality of the clone: The about 2250 sequences from the clone collection were sorted according to clones and clustered. If more than one contig was formed, the clone was designated 'Contamination'. The contigs and singletons were blasted against CDS plus pseudogenes from the TIGRv5 annotation, and the resulting AGI code is presented if more than 90 percent identity was found. The sequences were also blasted against all TIGRv5 introns, and matches longer than 50 bp with 95 percent identity are reported as 'intron found'. The remaining terms for SeqAnalysis describe the outcome of the evaluation of the CDS detected after pairwise alignment with CDS plus pseudogenes

from the TIGR5 annotation file. The sequences or contigs for which a full CDS with or without STOP codon was detected, a BLASTp against all TIGR5 protein sequences was performed. Full perfect: 100 percent identity; full good: better than 95 percent identity over more than 95 percent of the sequence; partial good: better than 95 percent identity over less than 95 percent of the sequence; weak similarity: less than 95 percent identity over less than 95 percent of the sequence; no similarity: no hit from BLASTp. Note that the collection contains a few clones for which sequencing was not successful, which could have simple technical reasons. Obviously, information about these clones is missing in the submitted data.

Insert Length: 896 Std Error: 0.00  
Seq primer: selB GTAACATCAGAGATTTTGAGACAC.

**FEATURES**

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i. 8396
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/note="Vector: pDONR201; in project REGIA (OLG-T01199-00876 Paz-Ares), a set of transcription factors generated. The ORFs were produced in the labs of the participants. generated by RT-PCR using cDNA from tissues as a template. Initially yeast recombination to move the vectors into target constructs. Of the clones contain 'REGIA' tag: 5pr-ATTTCAGCTCACCACC-3pr; RG tag: 5pr-CATGCCAATTCGGGATC-3pr. In project, the Gateway system because all ORFs were transferred into Gateway. For end-sequencing at the DINA. For end-sequencing at the DINA. MPI of Plant Breeding Research (Weisshaar), the plasmids were DH5alpha, arrayed into 96-well plates was prepared. Re-transformation because a number of clones displayed submission has been handled by GABI (http://gabi.rzd.de)."
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## ORIGIN

Query Match	36.5%	Score 344.2	DB 10	Length 896
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QY	162	AAGTCACCTTTCTCAAAAGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGTTTCCTTC	221	
DB	631	AAGTCACCTTTCTCAAAACGACGCNAATGGTCTCATCGAGAAAGCTCGACAACTTTTCAATTC	572	
QY	222	TCTGTGACGCATCGTCGGCTCTTCTCGTCGTCTCGGCTCGGCAAGCTCTACAGCTTCT	281	
DB	571	TCTGTGNAATCTTCCATCGCTGTTCTCGTCGTCTCGGCTCGGNAAACTCTACAAGCTCG	512	
QY	282	CCTCGGCGGATAACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATC	341	
DB	511	CCTCGGTCGACACATGTCAAAGATCATTTGATCGTTACGAAATACATCATGCTGATGAAC	452	
QY	342	TTAAAGCCTTGGATCATCATGTCAAAAGCTCTGAACCTATGGTTTCACTATGAGGACTCTTG	401	
DB	451	TTGAAGCCTTTAGATCTTTCGAGAAAAAACTCGGAATTATCTGCCACTCAAGAGGTTACTAG	392	

Qy	402	AACTTGGGATAGCAGACTTGTGGGATCAAAATGTCACAAATGTGAGTATCGATGCTCTTG	461
Db	391	AAATAGTCCAAAGCAAGCTTGAAGAATCAAAATGTCATATATGCAAGTGTGGAATCTTAA	332
Qy	462	TTCAACTGGAGGAGAACCTTGGAGACTGCGCTCTCCGTGACTAGAGCCAGAGACCGNAC	521
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Qy	582	AGGTTTGGCTAGCCAGATGGAGAAATCATCATGTGGGAGCAGAACTGAGATGGAGA	641
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Qy	642	TGTCACCTGCTGACAAATCTCCGACAACTTCCGGTGACTCTCCCACTACTTAATTAGC	701
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Qy	702	CACCTTAAATCGCGGTTGAAA	723
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CN828657 679 bp mRNA linear EST 14-MAY-2005

EL3007R Brassica embryo library (EL) Brassica napus cDNA clone

EL3007 5', mRNA sequence.

CN828657

CN828657.1 GI:65298443

EST.

Brassica napus (rape)

Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 679)

Sharpe,A.G., Gjetvaj,B., Durkin,J. and Lydiate,D.J.

Brassica napus ESTs

Unpublished (2004)

Contact: Sharpe, A.G.

Molecular Genetics

Agriculture & Agri-Food Canada

107 Science Place, Saskatoon, Saskatchewan, Canada, S7N0X2

Tel: 306 956 7271

Fax: 306 956 7247

Email: sharpea@agr.gc.ca

Seq primer: T7.

Location/Qualifiers

1..679

/organism="Brassica napus"

/mol\_type="mRNA"

/cultivar="DH12075 (double haploid line from Cresor x Westar cross)"

/db\_xref="taxon:3708"

/clone="EL3007"

/dev\_stage="Mid to late embryos (4-6 mg)"

/lab\_host="E. coli Electromax DHS alpha-e

/lab\_lib="Brassica embryo library (EL)"

/note="Organ: Embryos without seed coat; Vector: pSPORT1 (modified: GCGCGCCG\*GACTAGTGAGTC\*cgagcggggTCGAC); Site\_1: NotI; Site\_2: SalI; Seeds were collected by Dr. Francois Ouellet when they were still very green (mid to large stage, cotyledons were formed). The seed coats were removed and the remaining tissue was used for cDNA library construction. mRNA was poly-A primed using SuperScript Plasmid System cDNA Synthesis and Cloning kit (Invitrogen) After initial screening, the most abundant redundant clones were screened out using 22 oligos designed to match napins (including albumins), cruciferins, oleosins, trypsin inhibitor 2, cytosolic GAPDH, cyclophilins, HSP70,

RESULT 15

CN828657

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

ORIGIN	deaturase, and CAB (LHCP). "
Query Match	35.9%; Score 338.4; DB 8; Length 679;
Best Local Similarity	77.5%; Pred. No. 4.2e-76;
Matches 423; Conservative	0; Mismatches 121; Indels 2; Gaps 1;
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Db	86 ACATCAGACTCAAAATTATGGGCATAAAGCCCTTGTGCGAAGACGAGCCATGGGAGAGAA 145
Qy	123 AACTAGAAATCAACGGGAATTGAGAACAAAGTAGCCGACAGTCACTTCTCCAAACGTC 182
Db	146 AAGTAGAGATCAAACTAATTAGAAACAAAGTAGTAGCAAGTCACCTTTCTCTAAACGAC 205
Qy	183 GCAACGGTCTCATCGAGAAAGCTCGTCAGACTTTCTGTTCTCTGTGAGCATCCGTCGCTC 242
Db	206 GCATGGTCTCATCGAGAAAGCTCGACAGCTTTCAGTTCTCTGTGAAATCATCCGTCGCTG 265
Qy	243 TTCTCGTCGTCCTCGCCTCGCGCAAGCTCTACAGCTTCTCTCTCGGCGAATAACCTGGTCA 302
Db	266 TTCTCGTCGTCCTCGCCTCTGGAATACTTACAACTCTCTCTTCGGGTGACAAATGACCA 325
Qy	303 AGATCCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCAGT 362
Db	326 ACATCATCGATCGTTATGGGCATACAAATGCTGTGAACTTTAGAAGCTTTGAATCTTCGAG 385
Qy	363 CAAAAGCTCTGAACTATGTTTCACTATGAGCTACTTGAACCTTGTGATAGCAAGCTTG 422
Db	386 AAAAACTCGGAGTTATCTTCCACACAATGAGTTACTCGAATCAGTCANAAAGCAATCTTG 445
Qy	423 TGGGATCAAAATGTCAAAAATGTGAGTATCGATGCTCTTGTGTTCAACTGGAGGAAACACCTTG 482
Db	446 AAGAAATCAAAATGTCGACAAAGTAAGTGTAGATTCTCTAAATTTCTCTGGAGGACCAGCTCG 505
Qy	483 AGACTGCGCTCTCGTGCATCTAGAGCCAAAGACCGAACTCATGTTTGAAGCTTTGTTGAGA 542
Db	506 AAACCTGCTCTGTCTGCAACTTAGAGCTTAGGAAGCAGAACTAAACGATGGAGTTTGTGAGA 565
Qy	543 ATCTTAAAGAAAAGGAGAAAATGCTGAAAGAAAGAACACAGGTTTTTCGCTAGCCAGATGG 602
Db	566 TGCTTCAAGAAAGGAGGAGTTGCTGTAGAGAAAGAAATCTTGTTTTGGCTTAGCCAGATAG 625
Qy	603 AGAATA 608
Db	626 GGAAAA 631

Search completed: May 22, 2006, 08:17:47  
Job time : 4487 secs

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2006, 05:53:02 ; Search time 253 Seconds  
(without alignments)  
6974.133 Million cell updates/sec

Title: US-09-857-346A-2  
Perfect score: 943  
Sequence: 1 cggaaagagaaaaaa.....tgagaaaaaa 943

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*

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- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7 COMB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H COMB.seq.\*
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- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP COMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE COMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	784.4	83.2	797	3	US-09-513-775B-1
2	448.6	47.6	867	3	US-09-513-775B-9
3	439	46.6	863	3	US-09-513-775B-7
4	324.4	34.4	687	3	US-09-853-450-39
5	324.4	34.4	907	3	US-09-513-775B-3
6	317.6	33.7	769	3	US-09-513-775B-5
7	297.8	31.6	579	3	US-09-853-450-49
8	148.6	15.8	7200	3	US-09-853-450-48
9	127.6	13.5	1294	4	US-09-869-582-4
10	127.6	13.5	1303	4	US-09-869-582-16
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13	123	13.0	1374	4	US-09-869-582-15
14	119.4	12.7	753	3	US-09-853-450-29
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16	111.6	11.8	1345	3	US-08-659-188-7
17	111.6	11.8	1345	3	US-08-655-241-7
18	111.6	11.8	1345	3	US-08-655-241-7
19	111.6	11.8	1345	3	US-09-149-976-7
20	111.6	11.8	1345	3	US-09-398-326-7
21	111.6	11.8	1345	3	US-09-853-450-7
22	104.2	11.0	1141	2	US-08-323-449B-1
23	104.2	11.0	1141	2	US-08-485-981-1

24	104.2	11.0	1141	2	US-08-867-087B-1	Sequence 1, Appli
25	104	11.0	1223	3	US-09-640-211A-32	Sequence 32, Appl
26	103.8	11.0	613	3	US-09-640-211A-2019	Sequence 2019, Ap
27	100.8	10.7	3589	4	US-09-869-582-2	Sequence 2, Appli
28	99.8	10.6	1054	2	US-08-576-156-1	Sequence 1, Appli
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31	99.8	10.6	1057	3	US-08-655-241-1	Sequence 1, Appli
32	99.8	10.6	1057	3	US-09-398-326-1	Sequence 1, Appli
33	99.8	10.6	1057	3	US-09-853-450-1	Sequence 1, Appli
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36	99.8	10.6	1220	4	US-09-869-582-13	Sequence 13, Appl
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44	99.2	10.5	5131	3	US-09-853-450-43	Sequence 43, Appl
45	97.8	10.4	1043	2	US-08-867-087B-12	Sequence 12, Appl

## ALIGNMENTS

## RESULT 1

US-09-513-775B-1  
; Sequence 1, Application US/09513775B  
; Patent No. 6693228  
; GENERAL INFORMATION:  
; APPLICANT: Amasino, Richard  
; APPLICANT: Schomburg, Fritz  
; APPLICANT: Michaels, Scott  
; APPLICANT: Sung, Si-Bum  
; TITLE OF INVENTION: Alteration of Flowering Time in Plants  
; FILE REFERENCE: 960396.96871  
; CURRENT APPLICATION NUMBER: US/09/513,775B  
; PRIOR FILING DATE: 2000-02-25  
; PRIOR APPLICATION NUMBER: 60/121,572  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: 60/123,455  
; PRIOR FILING DATE: 1999-03-05  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 797  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(588)  
US-09-513-775B-1

Query Match 83.2%; Score 784.4; DB 3; Length 797;

Best Local Similarity 99.9%; Pred. No. 3e-211;

Matches 785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	110	ATGGGAGAGAAAACTAGAAATCAAGCGNATTGAGACAAAAGTAGCCGCAAGTCACC	169
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Qy	170	TTCTCCAAAGCTCGCAACGGTCTCATCGAGAAAGCTGTCAGCTTTCTCTGTGAC	229
Db	61	TTCTCCAAAGCTCGCAACGGTCTCATCGAGAAAGCTGTCAGCTTTCTCTGTGAC	120
Qy	230	GCATCGTGGCTTCTCTCGTGGCTCGCGCAAGCTCTACAGCTTCTCTCGGC	289
Db	121	GCATCGTGGCTTCTCTCGTGGCTCGCGCAAGCTCTACAGCTTCTCTCGGC	180
Qy	290	GATACTCGTCAAGATCTTGTGATGATGGAACAGCATGCTGATGATCTTAAGCC	349

Db 181 GATAACCTGCTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCC 240  
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Db 241 TTGGATCATCAGTCAAAAGCTCTGAACATGTTGATGTTTCACTATGAGCTACTTGAACCTTTG 300  
QY 410 GATAGCAAGCTTGTGGATCAAAATGTCAAAATGTCAGATATGATGCTCTTGTTCACACTG 469  
Db 301 GATAGCAAGCTTGTGGATCAAAATGTCAAAATGTCAGATATGATGCTCTTGTTCACACTG 360  
QY 470 GAGGAACACCTTCAGACTGCCCTCTCCGTGACTAGAGCCCAAGAGACCGAAGCTCATGTTG 529  
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QY 530 AAGCTTGTGAGATCTTAAAGAAAAGGAGAAAATGCTGAAGAGAGAACCAAGGTTTGG 589  
Db 421 AAGCTTGTGAGATCTTAAAGAAAAGGAGAAAATGCTGAAGAGAGAACCAAGGTTTGG 480  
QY 590 GCTAGCCAGATGAGAAATATCATCATGTTGGAGCAGAAAGCTGAGATGAGATGTCACCT 649  
Db 481 GCTAGCCAGATGAGAAATATCATCATGTTGGAGCAGAAAGCTGAGATGAGATGTCACCT 540  
QY 650 GCTGGCAAAATCTCCGACATCTTCCGGTGACTCTCCGACTTAAATAGCCACCTTAA 709  
Db 541 GCTGGCAAAATCTCCGACATCTTCCGGTGACTCTCCGACTTAAATAGCCACCTTAA 600  
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QY 830 AAGAGCTTGTGTTGATGATACTTAAAGTACGGAATCAAGTCACTATCTGTTTAAAG 889  
Db 721 AAGAGCTTGTGTTGATGATACTTAAAGTACGGAATCAAGTCACTATCTGTTTAAAG 780  
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## RESULT 2

US-09-513-775B-9

; Sequence 9, Application US/09513775B

; Patent No. 6693228

; GENERAL INFORMATION:

; APPLICANT: Amasino, Richard

; APPLICANT: Schomburg, Fritz

; APPLICANT: Michaels, Scott

; APPLICANT: Sung, Si-Bum

; TITLE OF INVENTION: Alteration of Flowering Time in Plants

; FILE REFERENCE: 960296.96871

; CURRENT APPLICATION NUMBER: US/09/513,775B

; CURRENT FILING DATE: 2000-02-25

; PRIOR APPLICATION NUMBER: 60/121,572

; PRIOR FILING DATE: 1999-02-25

; PRIOR APPLICATION NUMBER: 60/123,455

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 867

; TYPE: DNA

; ORGANISM: Brassica rapa

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(588)

US-09-513-775B-9

Query Match

Best Local Similarity 47.6%; Score 448.6; DB 3; Length 867;

84.2%; Pred. No. 2.1e-116;

Matches 543; Conservative 0; Mismatches 94; Indels 8; Gaps 3;  
QY 110 ATGGGAGAAAAAACTAGAAATCAAGCGAATTTGAGAAACAAAGTAGCCGACAAAGTCACC 169  
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QY 170 TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTCTCTGTGAC 229  
Db 61 TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTCTCTGTGAC 120  
QY 230 GCATCGCTCGCTTCTTCTGCTCTCCGCTCGGCAAGCTCTACAGCTTCTCTCTCGGC 289  
Db 121 GCATCTGTGTGGCTTCTTCTGCTCTCCGCTCCGACAAACTCTACAGCTTCTCTCTCGGC 180  
QY 290 GATAACCTGGTCAAGATCCCTGATGATGGAACACATGCTGATGATCTTAAAGCC 349  
Db 181 GATAGACTGGAGAAATCTTGTGATGATGGAACAAACATGCTGATGATCTCAATGCC 240  
QY 350 TTGGATCATCAGTCAAAAGCTCTGAACTATGTTTCACTATGAGCTACTTGAACCTTTG 409  
Db 241 CTGGATCTTCACTCAAAATCTCTGAACTATAGTTCACACCATGAGCTACTAGAACTTTG 300  
QY 410 GATAGCAAGCTTGTGGATCAAAATGTCAAAATGTCAGATATGAGTATGATGCTCTTGTTCAACTG 469  
Db 301 GAAAGCAAGCTTGTGGAATCAATTG---ATGATGTAAGCGTGGATTCCCTCGTTGAGCTA 357  
QY 470 GAGGAACACCTTCAGACTGCCCTCTCCGTGACTAGAGCCCAAGAGACCGAAGCTCATGTTG 529  
Db 358 GAAGATCACTTGGAGACTGCCCTCTCTGTAAGCTGAGCTCGGAAGCGAAGCTTAATGTTA 417  
QY 530 AAGCTTGTGGAATCTTAAAGAAAAGGAGAAAATGCTGAAAAGAGAGAACCAAGGTTTGG 589  
Db 418 AAGCTTGTGGAAGCTCTCAAGAAAAGGAGAAATCTGCTGAAAAGAGAGAACCAAGGTTTGG 477  
QY 590 GCTAGCCAGATGAGAAATATCATCATGTTGGAGCAGAAAGCTGAGATGAGATGTCACCT 649  
Db 478 GCTAGCTCAGATTTGAGAGAAAATCTTGAAGGAGCGAAGCTGATAATATAGAGATGTCA 537  
QY 650 GCTGGACAAATCTCCGA---CAATCTTCGGTGACTCTCCCACTACTTAAATAGCCACCT 706  
Db 538 TCTGGACAAATCTCCGACATCAATCTTCTGTAATCTCCCGCTGCTTAAATTAACCACT 597  
QY 707 TAAATCGCGGTTGAAATCAAAATCAAAACATATATATATGA 751  
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## RESULT 3

US-09-513-775B-7

; Sequence 7, Application US/09513775B

; Patent No. 6693228

; GENERAL INFORMATION:

; APPLICANT: Amasino, Richard

; APPLICANT: Schomburg, Fritz

; APPLICANT: Michaels, Scott

; APPLICANT: Sung, Si-Bum

; TITLE OF INVENTION: Alteration of Flowering Time in Plants

; FILE REFERENCE: 960296.96871

; CURRENT APPLICATION NUMBER: US/09/513,775B

; CURRENT FILING DATE: 2000-02-25

; PRIOR APPLICATION NUMBER: 60/121,572

; PRIOR FILING DATE: 1999-02-25

; PRIOR APPLICATION NUMBER: 60/123,455

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 863

; TYPE: DNA

; ORGANISM: Brassica rapa

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(588)

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; LENGTH: 687
; TYPE: DNA

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; LENGTH: 687
; TYPE: DNA

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FEATURE:	NAME/KEY
1. <b>High-Speed Internet</b>	1. <b>High-Speed Internet</b>
2. <b>Free Parking</b>	2. <b>Free Parking</b>
3. <b>24-Hour Security</b>	3. <b>24-Hour Security</b>
4. <b>Pet-Friendly</b>	4. <b>Pet-Friendly</b>
5. <b>Stainless Steel Appliances</b>	5. <b>Stainless Steel Appliances</b>
6. <b>Hardwood Floors</b>	6. <b>Hardwood Floors</b>
7. <b>Walk-In Closets</b>	7. <b>Walk-In Closets</b>
8. <b>Central Air Conditioning</b>	8. <b>Central Air Conditioning</b>
9. <b>Gated Community</b>	9. <b>Gated Community</b>
10. <b>Storage Units Available</b>	10. <b>Storage Units Available</b>
11. <b>Proximity to Schools</b>	11. <b>Proximity to Schools</b>
12. <b>Close to Shopping Centers</b>	12. <b>Close to Shopping Centers</b>
13. <b>Modern Kitchen</b>	13. <b>Modern Kitchen</b>
14. <b>Open Floor Plan</b>	14. <b>Open Floor Plan</b>
15. <b>Large Backyard</b>	15. <b>Large Backyard</b>
16. <b>Double Garage</b>	16. <b>Double Garage</b>
17. <b>Energy-Efficient Windows</b>	17. <b>Energy-Efficient Windows</b>
18. <b>Granite Countertops</b>	18. <b>Granite Countertops</b>
19. <b>Walk-In Pantry</b>	19. <b>Walk-In Pantry</b>
20. <b>Master Suite with Walk-In Closet</b>	20. <b>Master Suite with Walk-In Closet</b>
21. <b>Hardwood Floors Throughout</b>	21. <b>Hardwood Floors Throughout</b>
22. <b>Stainless Steel Appliances</b>	22. <b>Stainless Steel Appliances</b>
23. <b>Open Floor Plan</b>	23. <b>Open Floor Plan</b>
24. <b>Large Backyard</b>	24. <b>Large Backyard</b>
25. <b>Double Garage</b>	25. <b>Double Garage</b>
26. <b>Energy-Efficient Windows</b>	26. <b>Energy-Efficient Windows</b>
27. <b>Granite Countertops</b>	27. <b>Granite Countertops</b>
28. <b>Walk-In Pantry</b>	28. <b>Walk-In Pantry</b>
29. <b>Master Suite with Walk-In Closet</b>	29. <b>Master Suite with Walk-In Closet</b>
30. <b>Hardwood Floors Throughout</b>	30. <b>Hardwood Floors Throughout</b>

FEATURE:	NAME/KEY
1. <b>High-Speed Internet</b>	1. <b>High-Speed Internet</b>
2. <b>Free Parking</b>	2. <b>Free Parking</b>
3. <b>24-Hour Security</b>	3. <b>24-Hour Security</b>
4. <b>Pet-Friendly</b>	4. <b>Pet-Friendly</b>
5. <b>Stainless Steel Appliances</b>	5. <b>Stainless Steel Appliances</b>
6. <b>Hardwood Floors</b>	6. <b>Hardwood Floors</b>
7. <b>Walk-In Closets</b>	7. <b>Walk-In Closets</b>
8. <b>Central Air Conditioning</b>	8. <b>Central Air Conditioning</b>
9. <b>Gated Community</b>	9. <b>Gated Community</b>
10. <b>Proximity to Schools</b>	10. <b>Proximity to Schools</b>
11. <b>Close to Shopping Centers</b>	11. <b>Close to Shopping Centers</b>
12. <b>Storage Units Available</b>	12. <b>Storage Units Available</b>
13. <b>Energy-Efficient Windows</b>	13. <b>Energy-Efficient Windows</b>
14. <b>Modern Kitchen Fixtures</b>	14. <b>Modern Kitchen Fixtures</b>
15. <b>Spacious Living Areas</b>	15. <b>Spacious Living Areas</b>
16. <b>Large Backyards</b>	16. <b>Large Backyards</b>
17. <b>Swimming Pools</b>	17. <b>Swimming Pools</b>
18. <b>Community Events</b>	18. <b>Community Events</b>
19. <b>Convenient Location</b>	19. <b>Convenient Location</b>
20. <b>Low Maintenance</b>	20. <b>Low Maintenance</b>

; LOCATION: (1)..(519)  
 US-09-513-775B-3

Query Match 34.4%; Score 324.4; DB 3; Length 907;  
 Best Local Similarity 77.3%; Pred. No. 2.5e-81;  
 Matches 394; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 110 ATGGGAAGAAAAAAGCTAGAAATCAAGCGAATTTGAGAACAAAGTAGCCGACAGTCACT 169  
 DB 1 ATGGGAAGAAAAAAGCTAGAAATCAAGCGAATTTGAGAACAAAGTAGCCGACAGTCACT 60

QY 170 TTCTCCAAAAGCTCGCAACGGTCTCATCGAAGAGCTCGTCAAGCTTTCTGTCTCTGTGAC 229  
 DB 61 TTCTCCAAAAGCTCGCAACGGTCTCATCGAAGAGCTCGTCAAGCTTTCTGTCTCTGTGAC 120

QY 230 GCATCCGTCGCT 289  
 DB 121 TCCTCCGTCGCT 180

QY 290 GATAACCTGGTCAAGATCCTTGCATCGAAGAGCTCTACAGCTTTCTGTCTCTCTCTCTCT 349  
 DB 181 GACGACATTTCCAAAGATCATTCGTTATGAAATACAACTGCTGATGAATCTCTCTCTCTCT 240

QY 350 TTGGATCATCTGCAAGCTCTGAACTATGTTGCACTATGAGCTTCTGAACTTTGTTG 409  
 DB 241 TTAGATCTTTGAAAGAAAAAATTCAGAAATATCTTCCACACAAGAGGTTACTAGAAACAGTC 300

QY 410 GATAGCAAGCTTTGGGATCAAAATGTCGAAATGAGTATGAGTATGAGTATGAGTATGAGT 469  
 DB 301 CAAGCAAGCTTTGAAAGAAATCAATGTCGAAATGTCGAAATGTCGAAATGTCGAAATGTCG 360

QY 470 GAGGAACACTTTGAGACTGCT 529  
 DB 361 GAGGAACACTTTGAGACTGCT 420

QY 530 AGCTTTGTTGAGAAATCTTAAGAAAGGAGAAATGCTGAAAGAGAGAACAGTCTTTG 589  
 DB 421 GAGTATATCGAGTCCCTTAAAGAAAGGAGAAATGCTGAGAGAGAGAACAGTCTTTG 480

QY 590 GCTAGCCAGATGGAGAAATATCATCATG 619  
 DB 481 GCTAGCCAGATGGAGAAATATCATCATG 510

RESULT 6  
 US-09-513-775B-5  
 ; Sequence 5, Application US/09513775B  
 ; Patent No. 6693228  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Amasino, Richard  
 ; APPLICANT: Schomburg, Fritz  
 ; APPLICANT: Michael, Scott  
 ; APPLICANT: Sung, Si-Bun  
 ; TITLE OF INVENTION: Alteration of Flowering Time in Plants  
 ; FILE REFERENCE: 960296.96871  
 ; CURRENT APPLICATION NUMBER: US/09/513,775B  
 ; CURRENT FILING DATE: 2000-02-25  
 ; PRIOR APPLICATION NUMBER: 60/121,572  
 ; PRIOR FILING DATE: 1998-02-25  
 ; PRIOR APPLICATION NUMBER: 60/123,455  
 ; PRIOR FILING DATE: 1999-03-05  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 769  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(534)  
 US-09-513-775B-5

Query Match 33.7%; Score 317.6; DB 3; Length 769;  
 Best Local Similarity 70.6%; Pred. No. 6.5e-74;  
 Matches 417; Conservative 0; Mismatches 162; Indels 12; Gaps 1;

QY 110 ATGGGAAGAAAAAAGCTAGAAATCAAGCGAATTTGAGAACAAAGTAGCCGACAGTCACT 169  
 DB 1 ATGGGAAGAAAAAAGCTAGAAATCAAGCGAATTTGAGAACAAAGTAGCCGACAGTCACT 60

QY 170 TTCTCCAAAAGCTCGCAACGGTCTCATCGAAGAGCTCGTCAAGCTTTCTGTCTCTGTGAC 229  
 DB 61 TTCTCCAAAAGCTCGCAACGGTCTCATCGAAGAGCTCGTCAAGCTTTCTGTCTCTGTGAC 120

QY 230 GCATCCGTCGCT 289  
 DB 121 TCCTCCGTCGCT 180

QY 290 GATAACCTGGTCAAGATCCTTGCATCGAAGAGCTCTACAGCTTTCTGTCTCTCTCTCTCT 349  
 DB 181 GACGACATTTCCAAAGATCATTCGTTATGAAATACAACTGCTGATGAATCTCTCTCTCTCT 240

QY 350 TTGGATCATCTGCAAGCTCTGAACTATGTTGCACTATGAGCTTCTGAACTTTGTTG 409  
 DB 241 TTAGATCTTTGAAAGAAAAAATTCAGAAATATCTTCCACACAAGAGGTTACTAGAAACAGTC 300

QY 410 GATAGCAAGCTTTGGGATCAAAATGTCGAAATGAGTATGAGTATGAGTATGAGTATGAGT 469  
 DB 301 CAAGCAAGCTTTGAAAGAAATCAATGTCGAAATGTCGAAATGTCGAAATGTCGAAATGTCG 360

QY 470 GAGGAACACTTTGAGACTGCT 529  
 DB 361 GAGGAACACTTTGAGACTGCT 420

QY 530 AGCTTTGTTGAGAAATCTTAAGAAAGGAGAAATGCTGAAAGAGAGAACAGTCTTTG 589  
 DB 421 GAGTATATCGAGTCCCTTAAAGAAAGGAGAAATGCTGAGAGAGAGAACAGTCTTTG 480

QY 590 GCTAGCCAGATGGAGAAATATCATCATG 619  
 DB 481 GCTAGCCAGATGGAGAAATATCATCATG 508

RESULT 7  
 US-09-853-450-49  
 ; Sequence 49, Application US/09853450  
 ; Patent No. 6828478  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yanofsky, Martin P.  
 ; APPLICANT: Pelaz, Soraya  
 ; APPLICANT: Ditta, Gary  
 ; APPLICANT: The Regents of the University of California  
 ; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants  
 ; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development  
 ; FILE REFERENCE: 19452A-002400US  
 ; CURRENT APPLICATION NUMBER: US/09/853,450  
 ; CURRENT FILING DATE: 2001-05-09  
 ; NUMBER OF SEQ ID NOS: 61  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 49  
 ; LENGTH: 579  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(579)  
 ; OTHER INFORMATION: alternatively spliced AGL27  
 US-09-853-450-49

Query Match 31.6%; Score 297.8; DB 3; Length 579;  
 Best Local Similarity 70.6%; Pred. No. 6.5e-74;  
 Matches 417; Conservative 0; Mismatches 162; Indels 12; Gaps 1;

QY 110 ATGGGAAGAAAAAAGCTAGAAATCAAGCGAATTTGAGAACAAAGTAGCCGACAGTCACT 169  
 DB 1 ATGGGAAGAAAAAAGCTAGAAATCAAGCGAATTTGAGAACAAAGTAGCCGACAGTCACT 60

QY 170 TTCTCCAAAAGCTCGCAACGGTCTCATCGAAGAGCTCGTCAAGCTTTCTGTCTCTGTGAC 229  
 DB 61 TTCTCCAAAAGCTCGCAACGGTCTCATCGAAGAGCTCGTCAAGCTTTCTGTCTCTGTGAC 120

QY 230 GCATCCGTCGCT 289  
 DB 121 TCCTCCGTCGCT 180

QY 290 GATAACCTGGTCAAGATCCTTGCATCGAAGAGCTCTACAGCTTTCTGTCTCTCTCTCTCT 349  
 DB 181 GACGACATTTCCAAAGATCATTCGTTATGAAATACAACTGCTGATGAATCTCTCTCTCTCT 240

QY 350 TTGGATCATCTGCAAGCTCTGAACTATGTTGCACTATGAGCTTCTGAACTTTGTTG 409  
 DB 241 TTAGATCTTTGAAAGAAAAAATTCAGAAATATCTTCCACACAAGAGGTTACTAGAAACAGTC 300

QY 410 GATAGCAAGCTTTGGGATCAAAATGTCGAAATGAGTATGAGTATGAGTATGAGTATGAGT 469  
 DB 301 CAAGCAAGCTTTGAAAGAAATCAATGTCGAAATGTCGAAATGTCGAAATGTCGAAATGTCG 360

QY 470 GAGGAACACTTTGAGACTGCT 529  
 DB 361 GAGGAACACTTTGAGACTGCT 420

QY 530 AGCTTTGTTGAGAAATCTTAAGAAAGGAGAAATGCTGAAAGAGAGAACAGTCTTTG 589  
 DB 421 GAGTATATCGAGTCCCTTAAAGAAAGGAGAAATGCTGAGAGAGAGAACAGTCTTTG 480

QY 590 GCTAGCCAGATGGAGAAATATCATCATG 617  
 DB 481 GCTAGCCAGATGGAGAAATATCATCATG 508





Db 740 ACCTTTGAATTCAAAGGAGTTAGACGAGCTTGAGCGTCAACTGCGGCTCTCTCAAGCA 799  
QY 499 GACTAGAGCCAAAGAACCGAATCATGTTGAAGCTTTGTTGAGAACTCTTAAAGAAAGGA 558  
Db 800 AGTTCGGTCCATCAAGACACAGTACATGCTTGACCGCTCTCGGATCTTCAAAATAAGA 859  
QY 559 GAAATCTGAAAGAGAGAACCAAGGTTTTGGCTAGCCAGATGGAGAAATATCATCATGT 618  
Db 860 GCAATGTTGCTTGAAACCAATAGAGCTTTGGCAATGAAGCTGGATGATGATGGTGT 919  
QY 619 GGGG 622  
Db 920 GAGA 923

## RESULT 10

US-09-869-582-16  
; Sequence 16, Application US/09869582  
; Patent No. 6987214  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Methods of Suppressing Flowering in Transgenic Plants  
; FILE REFERENCE: 19452A-002210US  
; CURRENT APPLICATION NUMBER: US/09/869,582  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR FILING DATE: 1999-10-15  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 1303  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; OTHER INFORMATION: AGL2 cDNA  
; NAME/KEY: CDS  
; LOCATION: (396)..(1142)  
; OTHER INFORMATION: AGL2  
US-09-869-582-16

Query Match 13.5%; Score 127.6; DB 4; Length 1303;  
Best Local Similarity 54.4%; Pred. No. 1.1e-25;  
Matches 296; Conservative 0; Mismatches 224; Indels 24; Gaps 1;

QY 103 AGAAGCCATGGGAAGAAAACCTAGAAATCAAGCGAATTGAGAACAAAGTAGCCGACA 162  
Db 389 AAAAGAAATGGGAAGGAGAGTAGAGCTGAAGAGGATAGAGAACAAATCAACAGCA 448  
QY 163 AGTCACCTTCTCAAAGCTCGAACGGTCTCATCGAGAAAGCTCGTCAGCTTCTGTCT 222  
Db 449 AGTAAGCTTTGCAAGCGTAGGAACGGTTGTTGAAAGAAAGCTTATGAATTTGTCTGT 508  
QY 223 CTGTGAGCATCGTCT 282  
Db 509 CTGTGAGCTGAAGTGTCTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 568  
QY 283 CTCGGCGATAAATCTGGTCAAGATCTCTGATCATATGAGAAACAGCATGCTGATCAT 342  
Db 569 CAGCTCTCAAAACATGCTCAAGACATTTGATCGGTACCAAGAAATGAGCTATGATCCAT 628  
QY 343 TAAAGCTTTGGATCATCAGTCAAAAG-----CTCTGAACATA 378  
Db 629 TGAAGTCAACAAACACCTGCCAAAGAACTTGAGAACAGCTACAGAGAAATATCTGAAGCT 688  
QY 379 TGGTTACACATATGAGTACTTCAACTTGTGGATAGCAAGCTTGTGGATCAAAATCTCAA 438  
Db 689 TAAGGGTAGATATGAGAACCTTCAACGTCAACAGAGAAATCTTCTTTGGGAGGATTTAGG 748  
QY 439 AAATGTGATGATCGATGCTCTTGTTCAACTGGAGGAACACCTTGGAGACTGCCCTCTCCGT 998

Db 749 ACCTTTGAATTCAAAGGAGTTAGACGAGCTTGAGCGTCAACTGCGGCTCTCTCAAGCA 808  
QY 499 GACTAGAGCCAAAGAACCGAATCATGTTGAAGCTTTGTTGAGAACTCTTAAAGAAAGGA 558  
Db 809 AGTTCGGTCCATCAAGACACAGTACATGCTTGACCGCTCTCGGATCTTCAAAATAAGA 868  
QY 559 GAAATCTGAAAGAGAGAACCAAGGTTTTGGCTAGCCAGATGGAGAAATATCATCATGT 618  
Db 869 GCAATGTTGCTTGAAACCAATAGAGCTTTGGCAATGAAGCTGGATGATGATGGTGT 928  
QY 619 GGGG 622  
Db 920 GAGA 932

## RESULT 11

US-09-853-450-27  
; Sequence 27, Application US/09853450  
; Patent No. 6828478  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Pelaz, Soraya  
; APPLICANT: Ditta, Gary  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants  
; FILE REFERENCE: 19452A-002400US  
; CURRENT APPLICATION NUMBER: US/09/853,450  
; CURRENT FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 747  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(747)  
; OTHER INFORMATION: SEPALLAT1 (SEP1)  
US-09-853-450-27

Query Match 13.3%; Score 125.4; DB 3; Length 747;  
Best Local Similarity 54.4%; Pred. No. 3.5e-25;  
Matches 292; Conservative 0; Mismatches 221; Indels 24; Gaps 1;

QY 110 ATGGGAAGAAAACCTAGAAATCAAGCGAATTGAGAACAAAGTAGCCGACCAAGTACC 169  
Db 1 ATGGGAAGAGGAGAGTAGAGCTGAAGAGGATAGAGAACAAATCAACAGACAAAGTAACG 60  
QY 170 TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTCTCTCTCTCTGAC 229  
Db 61 TTGCAAAAGCGTAGGAACGGTTTGTGAAAGAAAGCTTATGAATTTGTCTCTCTGTAT 120  
QY 230 GCATCCGTCT 289  
Db 121 GTTGAAGTGTCTCTCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180  
QY 290 GATTAACCTGGTCAAGATCTTGTATGATATGAGAAACAGCATGCTGATGATCTTAAAGCC 349  
Db 181 TCAACATGCTCAAGACACTTGTATCGGTACCAAGAAATGAGCTATGATGATGATGATG 240  
QY 350 TTGGATCATCAGTCAAAAG-----CTCTGAACATATGTTCA 385  
Db 241 AACACAAACCTGCCAAAGAACTTGAGAACAGCTACAGAGAAATATCTGAAGCTTAAGGGT 300  
QY 386 CACTATGAGCTACTTGAACCTTGTGATAGCAAGCTTGTGGGATCAAAATGCTCAAAATGTG 445  
Db 301 AGATATGAGAACCTTCAACGTCACAGAGAAATCTTCTTGGGGAGGATTTAGGACCTTTG 360  
QY 446 AGTATCGATGCTTGTGTTCAACTGGAGGAACACCTTGGAGACTGCCCTCTCCGTGACTAG 505  
Db 361 AATTCAAAGGAGTTAGAGCAGCTTGGAGGCTCAACTGGAGCGGCTCTCTCAAGCAAGTTCGG 420

Qy	506	GC	CA	AG	AG	AG	AG	CG	GA	CT	CA	TG	TG	GA	AG	CT	T	T	AA	GA	AA	GA	GA	AA	AT	G	565						
Db	421	T	C	C	A	T	C	A	A	G	A	G	C	A	G	T	C	T	C	G	A	T	C	T	C	G	480						
Qy	566	CT	GA	AG	AA	GA	AA	CA	G	CT	T	T	T	G	CT	AG	CA	CA	G	AT	GG	GA	AA	T	A	AT	CA	T	CA	T	G	GA	622
Db	481	T	T	G	C	T	GA	AA	CA	AA	T	AG	AG	C	T	T	GG	CA	AT	GA	AG	C	T	GG	AT	GA	T	GA	T	GA	T	GA	537

**RESULT 12**

```

US-09-869-582-6
; Sequence 6, Application US/09869582
; Patent No. 6987214
; GENERAL INFORMATION:
; APPLICANT: Yancofsky, Martin P.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Methods of Suppressing Flowering in Transgenic Plants
; FILE REFERENCE: 19452A-002210US
; CURRENT APPLICATION NUMBER: US/09/869,582
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/104,604
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: WO PCT/US99/24407
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1349
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: AGL4 cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (339)..(1091)
; OTHER INFORMATION: AGAMOUS-LIKE 4 (AGL4)
US-09-869-582-6

```

Query Match	13.0%;	Score 123;	DB 4;	Length 1349;
Best local Similarity	53.5%;	Pred. No. 2.2e-24;		
Matches 298;	Conservative 0;	Mismatches 235;	Indels 24;	Gaps 1;

  

QY	76	AAATTAGGGCACAAGCCCTCTCGGAGAGAGCCATGGGAAGAAAAAACTAGAAATCAA	135
DB	305	AAATAAGATAGGATTTTTTGGGTGAGGAAGATGGGAAGAGAGATAGAGCTCAA	364
QY	136	GCGAATTGAGAACAAAAAGTAGCCAGACACCTTCTCCAAACGTCGCACCGCTCTCAT	195
DB	365	GAGGATAGAGAACAAAATCAACAGACAAAGTGACGTTTGCTAAACGTAGAAATCGTTTGCT	424
QY	196	CGAGAAAGCTCGTCAGCTTTCTGTTCTCTGTGACGCATCCGTCGCTCTTCTCGTCGTC	255
DB	425	GAATAAAAGCTTATGAGCTTTCTGTTCTCTGCGATGCTGAAGTCTCTCTCATCGCTTCTC	484
QY	256	CGCTCCGGCAAGCTCTACAGCTTCTCCTCCGGCGATAACCTGTCGAAGATCCTTGATCG	315
DB	485	CAACGTGGCAAGCTCTACGAGTTCTGAGCACTCCAAATGCTCAAGACACTGGAAAG	544
QY	316	ATATGGGAAAACGACATGCTGATGATCTTAAAGCCCTTGGATCATCAGTCAAAAAGCTCTGAA	375
DB	545	GTATCAGAAGTGTAGCTATGGCTCCA TTGAAGTCAACAAACCTGCTAAAGAGCTTGA	604
QY	376	CTATGGTT-----CACACTATGAGCTACTTGAACCTTGTTGGA	411
DB	605	GAACAGCTACAGAGAGTACTTGAAGCTGGAAGGTAGATATGAAAACTGCAACGTCAGCA	664
QY	412	TAGCAAGCTTTGTGGGATCAAAATGTCAAAAATGTGAGTATCGATGCTCTTGTTCAACTGGA	471
DB	665	GAGNAATCTTCTTGGAGAGGATCTTGGACCTCTGAAATTCAAAGGAGCTAGAGCAGCTTGA	724
QY	472	GGAAACACTTTGAGATGCGCCTCTCCGTTGACTAGAGCCAGAGACCGAACTCATGTTTGA	531

Db	725	CGCTCAACTAGACGCGCTCTCTGAAAGCAAGTTCCGTGCGATCAAGACACAGATATATGCTTGA	784
Qy	532	GCTTGTGAGAAATCTTAAAGAAAGGAGAAAATGCTGAAAGAGAGAACCAAGTTTGTGC	591
Db	785	CCAGCTCTCTGATCTTCAAGGTAAGGAGCATATCTTGTGTGATGCCACAGAGCTTTGTC	844
Qy	592	TAGCCAGATGGAGAATA	608
Db	845	AATGAAGCTGGAAGATA	861

**RESULT 13**

```

US-09-869-582-15
; Sequence 15, Application US/09869582
; Patent No. 6987214
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin P.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Methods of Suppressing Flowering in Transgenic Plants
; FILE REFERENCE: 19452A-002210US
; CURRENT APPLICATION NUMBER: US/09/869,582
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/104,604
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: WO PCT/US99/24407
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 1374
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: AGL4 CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (347)..(1099)
; OTHER INFORMATION: AGL4
US-09-869-582-15

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Query Match	13.0%;	Score 123;	DB 4;	Length 1374;	
Best Local Similarity	53.5%;	Pred. No. 2.3e-24;			
Matches 298;	Conservative	0;	Mismatches 235;	Indels 24;	Gaps 1;
QY	76	AAATTAGGCGACAAAGCCCTCTCGAGAGAGCCATGGGAAGAAAAAACTAGAAAACTAA	135		
DB	313	AAATATAGATAGGGATTTTTTGGGGTGAGGAAGATGGGAAGGAAGATGAGACTCA	372		
QY	136	GCGAATTGAGAAACAAAGTAGCGACAAAGTCACTTCTCCAAACGTCGCAACGGTCTCAT	195		
DB	373	GAGGATAGAGAACAAATAATCAACAGATGACGTTTGTCTAAACGTAGAAAATGGTTTGTCT	432		
QY	196	CGAGAAAGCTCGTCAGCTTTCGTTCTCTGTGAGCGATCCGTCGCTCTTCTCGTCGCTC	255		
DB	433	GAATAAAGCTTATGAGCTTTCTGTTCTCTCGATGCTGAAGTCTCTCTCATGCTCTCTC	492		
QY	256	CGCTCCGGCAAGCTCTACAGCTTCTCTCCGGCGATTAACCTGGTCAAGATCTCTGATCG	315		
DB	493	CAACCGTGGCAAGCTCTACGAGTTCTGACGACCTCCCAACATGCTCAAGACACTGGAAAG	552		
QY	316	ATATGGGAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCAGTCAAAAGCTCTGAA	375		
DB	553	GTATCAGAAGTGTAGCTATGGCTCCATTGAAGTCAACAAACCTGCTTAAAGAGCTTGA	612		
QY	376	CTATGTTT-----CACACTATGAGCTACTTGAACCTTGTGGA	411		
DB	613	GAACAGCTACAGAGAGTACTTGAAGCTGAAAAGGTAGATATGAAAACTGCAACGTACGA	672		
QY	412	TAGCAAGCTTGTGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCAACTGGA	471		
DB	673	GAGAAATCTCTTTGGAGAGGATCTTGGACCTCTGAAATCAAAGGAGCTAGAGCAGCTTGA	732		
QY	472	GGAAACCTTGAAGCTGCCCTCTCCGTGACTAGAGCCAAAGAACCGAACTCATGTTGAA	531		

Db 733 GCCTCACTAGACGGCTCTCTGAAGCAAGTTGCTGCATCAAGACACAGTATATGCTTGA 792  
Qy 532 GCTTGTGAGAACTTAAAGAAAGGAGAAATGCTGAAAGAGAGAACCAAGTTTGGC 591  
Db 793 CCAGCTCTCTGATCTTCAAGGTAAAGGACATATCTTGTCTTGAATGCCAACACAGAGCTTTGTC 852  
Qy 592 TAGCCAGATGGAGAATA 608  
Db 853 AATGAAGCTGGAAGATA 869

## RESULT 14

US-09-853-450-29  
; Sequence 29, Application US/09853450  
; Patent No. 6828478  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin P.  
; APPLICANT: Pelaz, Soraya  
; APPLICANT: Ditta, Gary  
; TITLE OF INVENTION: The Regents of the University of California  
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants  
; FILE OF INVENTION: Exhibiting Modulated Reproductive Development  
; FILE REFERENCE: 19452A-002400US  
; CURRENT APPLICATION NUMBER: US/09/853,450  
; CURRENT FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 753  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(753)  
; OTHER INFORMATION: SBPALLATA2 (SBP2)  
US-09-853-450-29

Query Match 12.7%; Score 119.4; DB 3; Length 753;  
Best Local Similarity 54.1%; Pred. No. 1.7e-23;  
Matches 283; Conservative 0; Mismatches 216; Indels 24; Gaps 1;  
Qy 110 ATGGGAAGAAAAAATACTAGAAATCAAGCGAATTTGAGAACAAAAGTAGCCGACAAAGTCACC 169  
Db 1 ATGGGAAGAGGAAGAGTAGAGCTCAAGAGGATAGAGAACAAAATCAACAGACAGTAGTGACG 60  
Qy 170 TTCTCAAAAGCTGCACCGCTCTATCGAGAAAGCTGTCAGCTTCTGTTCTCTGTGAC 229  
Db 61 TTTGCTAAACGTAGAAATGTTTGTCTGAAAAAAGCTTATGAGCTTCTGTTCTCTGCGAT 120  
Qy 230 GCATCGCTCGCTCTCTCTGCTGCTCTCGCTCCGCAAGCTCTACAGCTTCTCTCCCGG 289  
Db 121 GCTGAAGTCTCTCTATGCTTCTTCTCAACCGTGGCAAGCTCTACAGTCTTCTGACGAC 180  
Qy 290 GATAACCTGGTCAAGATCTTGTATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCC 349  
Db 181 TCCAAACATGCTCAAGACATCGAAAGGTATCAGAAAGTATCAGAAAGTATGCTGCTTGAAGTC 240  
Qy 350 TTGGATCATAGTCAAAAGCTCTGAAGTATGGTT-----CA 385  
Db 241 AACAAACAAACCTGTAAGAGCTTGAGAACAGCTACAGAGTACTTGAAGCTGAAAAGT 300  
Qy 386 CACTATGAGCTACTTGAACCTTGTGGATAGCAAGCTTGTGGGATCAAAATGCAAAATG 445  
Db 301 AGATATGAAAATCTGCACGTACAGCAGAAATCTTCTTGGAGAGATCTTGGACCTCTG 360  
Qy 446 AGTATCGATGCTCTTGTTCACATGGAGGAACACCTTGGAGACTGCCCTCTCCGTGACTAGA 505  
Db 361 AATTCAAAGAGCTAGAGCAGCTTGAGCGCTCAACTAGACGGCTCTCTGAAGCAAGTTCG 420  
Qy 506 GCCAAGAACCGAACTCATGTTGAGCTTGTGAGAAATCTTAAAGAAAGGAGAAATG 565  
Db 421 TGCATCAAGACACAGTATATGCTTGAACCAAGCTCTCTGATCTTCAAGGTAAAGGAGCATATC 480

Qy 566 CTGAAGAGAGAGAACCAAGCTTTTGGCTAGCCAGATGGAGAATA 608  
Db 481 TTGCTTGATGCCAACAGAGCTTTGTCAATGAAGCTGGAAGATA 523  
RESULT 15  
US-08-592-214A-7  
; Sequence 7, Application US/08592214A  
; Patent No. 5811536  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin P.  
; TITLE OF INVENTION: Cauliflower Floral Meristem Identify  
; TITLE OF INVENTION: Genes and Methods of Using Same  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/592,214A  
; FILING DATE: 26-JAN-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 1927  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1345 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1345  
; NAME/KEY: misc feature  
; LOCATION: 1..1345  
; OTHER INFORMATION: /note= "product = Zea mays AP1"  
US-08-592-214A-7

Query Match 11.8%; Score 111.6; DB 2; Length 1345;  
Best Local Similarity 52.6%; Pred. No. 3.7e-21;  
Matches 286; Conservative 0; Mismatches 234; Indels 24; Gaps 1;  
Qy 105 AAGCATCGGAAGAAAAAACTAGAAATCAAGCGAATTTGAGAACAAAAGTAGCCGACCAAG 164  
Db 144 AGGCGATCGGCGCGGCAAGGTACAGCTGAAGCGGTAGAGAACAAAGATAAACCCGCGAG 203  
Qy 165 TCACCTTCTCCAAAGCTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTTCTCT 224  
Db 204 TGACCTTCTCCAAAGCGCCGGAACGCGCTGCTCAAGAAAGCGCACGAGATCTCCGCTCT 263  
Qy 225 GTGAGCATCGTCTGCTCTTCTCGTCTGCTCGCTCCGCAAGCTCTACAGCTTCTCTCT 284  
Db 264 GCGATCGCGAGGTGCGCGCTCATGCTTCTTCTCCCAAGGCGAAGCTCTACGAGTAGCGA 323  
Qy 285 CCGCGGATPAACCTGGTCAAGATCCCTTGTATCGATATGGGAAACAGCATGCTGATGATCTTA 344  
Db 324 CCGACTCCCGCATGGACAAAATTTCTTGAACGCTATGAGCGATATTCCTATGCTGAAAAGG 383

Qy	345	AAGCCTTGGATCATCAGTCAAAAGCTCTGAAGTATGGTTTCACTA-----	390
Db	384	CTCTTATTTTCAGCTGAATCTGAAAGTGAGGGAAATTTGGTCCCGAATACAGGAACTGA	443
Qy	391	-----TGAGCTACTTGAACTTTGTGGATAGCAAGCTTGTGGGATCAAAATGTCAAAA	440
Db	444	AGGCCAAATTTGAGACCCATACAAAATGCCCAAGCACCTGATGGGAGGATCTAGAGT	503
Qy	441	ATGTGAGTATCGATGCTTTGTTCAACTGGAGGAAACACCTTGAGACTGCCCTCTCCGTGA	500
Db	504	CTTTGAATCCCAAAGAGCTCCAGCAACTTAGAGCAGCAGCTGGATAGCTCACTGAAGCACA	563
Qy	501	CTAGAGCCAAAGAACCGAATCATGTTGAAGCTTGTGAGAATCTTAAAGAAAAGGAGA	560
Db	564	TCAGATCAAGGAGAGAGCCACCTTATGSCCGAGTCTATTTCTGAGCTACAGAAAGGAGA	623
Qy	561	AAATGCTGMAAGAGAGAACAGGTTTTTGGCTAGCCAGATGGAGAAATATCATCATGTGG	620
Db	624	GGTCACTGCAGGAGAGAGAACAGGCTCTGCAGAAGGAACCTTGGGAGAGGCGAAGGCCG	683
Qy	621	GAGC 624	
Db	684	TCGC 687	

Search completed: May 22, 2006, 10:00:19  
 Job time : 256 secs

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Query Match		100.0%;	Score 943;	DB 7;	Length 943;
Best Local Similarity		100.0%;	Pred. No. 2.6e-246;		
Matches 943;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CGAGAAAGGAAAAAATAAGAGAGAAACGCTTAGTATCTCCGGCGACTTGAAC	60		
DB	1	CGAGAAAGGAAAAAATAAGAGAGAAACGCTTAGTATCTCCGGCGACTTGAAC	60		
QY	61	CCAAACCTGAGGATCAAAATAGGGCCAAAGCCCTCTCGGAGAGAGCCATGGGAAGAA	120		
DB	61	CCAAACCTGAGGATCAAAATAGGGCCAAAGCCCTCTCGGAGAGAGCCATGGGAAGAA	120		
QY	121	AAACTAGAAATCAAGGAATTGAGAACAAAGTAGCCGACAGTCACTTCTTCCAAACG	180		
DB	121	AAACTAGAAATCAAGGAATTGAGAACAAAGTAGCCGACAGTCACTTCTTCCAAACG	180		
QY	181	TCGCAAGGCTCATCGAGAAAGCTCGTCAGCTTCTGTCTCTGTGAGCGCATCCGTCGC	240		
DB	181	TCGCAAGGCTCATCGAGAAAGCTCGTCAGCTTCTGTCTCTGTGAGCGCATCCGTCGC	240		
QY	241	TCCTCTCGTCTCCGGCTCCGGCAAGCTCTACAGCTTCTCTCCGGCGATAACCTGGT	300		
DB	241	TCCTCTCGTCTCCGGCTCCGGCAAGCTCTACAGCTTCTCTCCGGCGATAACCTGGT	300		
QY	301	CAAGATCTTGTATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCA	360		
DB	301	CAAGATCTTGTATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCA	360		
QY	361	GTCAAGGCTCTGAATATGGTTTCACTATGAGCTACTTGAACCTTGTGATAGCAAGCT	420		
DB	361	GTCAAGGCTCTGAATATGGTTTCACTATGAGCTACTTGAACCTTGTGATAGCAAGCT	420		
QY	421	TGTGGATCAAAATGTCAAAATGTAGTATCGATGCTCTTGTTCACCTCGAGGAAACCT	480		
DB	421	TGTGGATCAAAATGTCAAAATGTAGTATCGATGCTCTTGTTCACCTCGAGGAAACCT	480		
QY	481	TGAGACTGCCCTCTCCGTGACTAGAGCCCAAGAGACCGAACTCATGTTGAAGCTTTGTA	540		
DB	481	TGAGACTGCCCTCTCCGTGACTAGAGCCCAAGAGACCGAACTCATGTTGAAGCTTTGTA	540		
QY	541	GAATCTTAAAGAAAGGAGAAATGCTGAAAGAGAGAACCGAGTTTGGCTAGCCAGAT	600		
DB	541	GAATCTTAAAGAAAGGAGAAATGCTGAAAGAGAGAACCGAGTTTGGCTAGCCAGAT	600		
QY	601	CGAGAAATATCATCATGTGCGAGCAGAACTGAGATGAGAGATGTCACTCTGGAACAAT	660		
DB	601	CGAGAAATATCATCATGTGCGAGCAGAACTGAGATGAGAGATGTCACTCTGGAACAAT	660		
QY	661	CTCCGACAACTTCCGGTGACTCTCCACTACTTAATTAGCCACCTTAAATCGGGGTTG	720		
DB	661	CTCCGACAACTTCCGGTGACTCTCCACTACTTAATTAGCCACCTTAAATCGGGGTTG	720		
QY	721	AAATCAAAATCCAAACATATATATATGAAGAAAAAATAAGATATGTAATTATT	780		
DB	721	AAATCAAAATCCAAACATATATATATGAAGAAAAAATAAGATATGTAATTATT	780		
QY	781	CGCTGATAAGGCGAGCGTTTGTATCTTAACTCTCTCTTTGGCCCAAGACTTTG	840		
DB	781	CGCTGATAAGGCGAGCGTTTGTATCTTAACTCTCTCTTTGGCCCAAGACTTTG	840		
QY	841	TGTGTGATCTTAAAGTAGCGAACTAAGTCAATACTATCTGTTTTAAGCAAAAGGTTG	900		
DB	841	TGTGTGATCTTAAAGTAGCGAACTAAGTCAATACTATCTGTTTTAAGCAAAAGGTTG	900		
QY	901	ATGAACCTTGTACTTATTTCGTGTGAGAAAAAATAAAAAA	943		
DB	901	ATGAACCTTGTACTTATTTCGTGTGAGAAAAAATAAAAAA	943		

RESULT 2  
US-10-374-780A-2129  
; Sequence 2129, Application US/10374780A  
; Publication No. US20040019927A1

GENERAL INFORMATION:  
; APPLICANT: Sherman, Bradley K  
; APPLICANT: Riechmann, Jose Luis  
; APPLICANT: Jiang, Cai-Zhong  
; APPLICANT: Heard, Jacqueline E  
; APPLICANT: Haake, Volker  
; APPLICANT: Creelman, Robert A  
; APPLICANT: Ratcliffe, Oliver  
; APPLICANT: Adam, Luc J  
; APPLICANT: Reuber, T. Lynne  
; APPLICANT: Keddle, James  
; APPLICANT: Broun, Pierre E  
; APPLICANT: Pilgrim, Marsha L  
; APPLICANT: Dubell III, Arnold T  
; APPLICANT: Pineda, Omaira  
; APPLICANT: Yu, Guo-Liang  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS  
; FILE REFERENCE: MBI-0047 CIP  
; CURRENT APPLICATION NUMBER: US/10/374,780A  
; CURRENT FILING DATE: 2003-02-25  
; PRIOR APPLICATION NUMBER: 09/837,944  
; PRIOR FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: 60/310,847  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/934,455  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/336,049  
; PRIOR FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/338,692  
; PRIOR FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: 10/171,468  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: 10/225,066  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: 10/225,067  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: 10/225,068  
; PRIOR FILING DATE: 2002-08-09  
; NUMBER OF SEQ ID NOS: 2906  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 2129  
; LENGTH: 943  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; OTHER INFORMATION: GL759 Predicted polypeptide sequence is paralogous to GL57, GB59,  
US-10-374-780A-2129

Query Match		100.0%;	Score 943;	DB 8;	Length 943;
Best Local Similarity		100.0%;	Pred. No. 2.6e-246;		
Matches 943;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CGAGAAAGGAAAAAATAAGAGAGAAACGCTTAGTATCTCCGGCGACTTGAAC	60		
DB	1	CGAGAAAGGAAAAAATAAGAGAGAAACGCTTAGTATCTCCGGCGACTTGAAC	60		
QY	61	CCAAACCTGAGGATCAAAATAGGGCCAAAGCCCTCTCGGAGAGAGCCATGGGAAGAA	120		
DB	61	CCAAACCTGAGGATCAAAATAGGGCCAAAGCCCTCTCGGAGAGAGCCATGGGAAGAA	120		
QY	121	AAACTAGAAATCAAGGAATTGAGAACAAAGTAGCCGACAGTCACTTCTTCCAAACG	180		
DB	121	AAACTAGAAATCAAGGAATTGAGAACAAAGTAGCCGACAGTCACTTCTTCCAAACG	180		
QY	181	TCGCAAGGCTCATCGAGAAAGCTCGTCAGCTTCTGTCTCTGTGAGCGCATCCGTCGC	240		
DB	181	TCGCAAGGCTCATCGAGAAAGCTCGTCAGCTTCTGTCTCTGTGAGCGCATCCGTCGC	240		
QY	241	TCCTCTCGTCTCCGGCTCCGGCAAGCTCTACAGCTTCTCTCCGGCGATAACCTGGT	300		
DB	241	TCCTCTCGTCTCCGGCTCCGGCAAGCTCTACAGCTTCTCTCCGGCGATAACCTGGT	300		
QY	301	CAAGATCTTGTATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCA	360		



Db 301 CAAGATCTTGCATCGATATGGAAACAGACAGCTGCTGATGATCTTAAAGCCTTGGATCATCA 360  
Qy 361 GTCAAAAGCTCTGAACCTATGTTTACACTATGAGCTACTTGAACCTTGTGGATAGCAAGCT 420  
Db 361 GTCAAAAGCTCTGAACCTATGTTTACACTATGAGCTACTTGAACCTTGTGGATAGCAAGCT 420  
Qy 421 TGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTCTTCAACTGGAGGAACACCT 480  
Db 421 TGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTCTTCAACTGGAGGAACACCT 480  
Qy 481 TGAGACTGCCCTCTCCGCTGACTAGAGCCAAAGAGACCGAACTCATGTTTGAAGCTTGTGA 540  
Db 481 TGAGACTGCCCTCTCCGCTGACTAGAGCCAAAGAGACCGAACTCATGTTTGAAGCTTGTGA 540  
Qy 541 GAATCTTAAAGAAAGAGAAATGCTGAAAGAGAGAACCAAGCTTTTGGCTAGCCAGAT 600  
Db 541 GAATCTTAAAGAAAGAGAAATGCTGAAAGAGAGAACCAAGCTTTTGGCTAGCCAGAT 600  
Qy 601 GGAGAAATATCATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACCTGCTGGACAAAT 660  
Db 601 GGAGAAATATCATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACCTGCTGGACAAAT 660  
Qy 661 CTCGACAAATCTCCGCTGACTCTCCCACTACTTAAATTTAGCCACCTTAAATCGCGGTTG 720  
Db 661 CTCGACAAATCTCCGCTGACTCTCCCACTACTTAAATTTAGCCACCTTAAATCGCGGTTG 720  
Qy 721 AAATCAAAATCCAAACATATATATTAATTAAGAGAAAAAATAAGATATGTAATTAAT 780  
Db 721 AAATCAAAATCCAAACATATATATTAATTAAGAGAAAAAATAAGATATGTAATTAAT 780  
Qy 781 CCGCTGATAGGGCGAGGCTTGTATATCTTAAATCTCTCTTCTTGGCCAGAGACTTTG 840  
Db 781 CCGCTGATAGGGCGAGGCTTGTATATCTTAAATCTCTCTTCTTGGCCAGAGACTTTG 840  
Qy 841 TGTGTGATCTTAAGTAGAGCGAACTAAGTCAATACTATCTGTTTAAAGACAAAGGTTG 900  
Db 841 TGTGTGATCTTAAGTAGAGCGAACTAAGTCAATACTATCTGTTTAAAGACAAAGGTTG 900  
Qy 901 ATGAACCTTTGACCTTATTCTGTGTGAGAAAAAATAAAAAA 943  
Db 901 ATGAACCTTTGACCTTATTCTGTGTGAGAAAAAATAAAAAA 943

RESULT 3

US-10-412-699B-1873  
; Sequence 1873, Application US/10412699B  
; Publication No. US20040045049A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendel Biotechnology, Inc.  
; APPLICANT: Zhang, James  
; APPLICANT: Fromm, Michael E.  
; APPLICANT: Heard, Jacqueline E.  
; APPLICANT: Riechmann, Jose Luis  
; APPLICANT: Adam, Luc J.  
; APPLICANT: Broun, Pierre E.  
; APPLICANT: Pineda, Omaliza  
; APPLICANT: Reuber, T. Lynne  
; APPLICANT: Keddie, James S.  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Jiang, Cai-Zhong  
; APPLICANT: Samaha, Raymond R.  
; APPLICANT: Pilgrim, Marsha L.  
; APPLICANT: Creelman, Robert A.  
; APPLICANT: Dubell, Arnold N.  
; APPLICANT: Ratcliffe, Oliver  
; APPLICANT: Kumimoto, Roderick  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants  
; FILE REFERENCE: MBI-0048CIP  
; CURRENT APPLICATION NUMBER: US/10/412,699B  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: 09/394,519

; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: 09/489,376  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: 09/506,720  
; PRIOR FILING DATE: 2000-02-17  
; PRIOR APPLICATION NUMBER: 09/533,030  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 09/533,392  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 09/533,029  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 09/532,591  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 09/533,648  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 09/713,994  
; PRIOR FILING DATE: 2000-11-16  
; PRIOR APPLICATION NUMBER: 09/819,142  
; PRIOR FILING DATE: 2001-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2011  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1873  
; LENGTH: 943  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-412-699B-1873

Query Match 100.0%; Score 943; DB 8; Length 943;  
Best Local Similarity 100.0%; Pred. No. 2,6e-246;  
Matches 943; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAGAAAGGAAAAAATAAGAGAGAAAAAGCTTAGTATCTCCGCGACTTGAAC 60  
Db 1 CGAGAAAGGAAAAAATAAGAGAGAAAAAGCTTAGTATCTCCGCGACTTGAAC 60  
Qy 61 CCAAACTGAGGATCAAAATTTAGGGCACAAGCCCTCTCGAGAGAACGATGGAGAA 120  
Db 61 CCAAACTGAGGATCAAAATTTAGGGCACAAGCCCTCTCGAGAGAACGATGGAGAA 120  
Qy 121 AAAAATAGAAATCAAGCGAAATTTAGAGACAAAGTAGCCGACAGCTTCTCCAAACG 180  
Db 121 AAAAATAGAAATCAAGCGAAATTTAGAGACAAAGTAGCCGACAGCTTCTCCAAACG 180  
Qy 181 TCGCAACGGTCTCATCGAGAAAGCTCGTCAAGCTTCTGTTCTCTGTGACGATCCGTCG 240  
Db 181 TCGCAACGGTCTCATCGAGAAAGCTCGTCAAGCTTCTGTTCTCTGTGACGATCCGTCG 240  
Qy 241 TCTTCTGCTGCTCTCCGCTCCGCGCAAGCTCTACAGCTTCTCTCCGCGGATACCTGGT 300  
Db 241 TCTTCTGCTGCTCTCCGCTCCGCGCAAGCTCTACAGCTTCTCTCCGCGGATACCTGGT 300  
Qy 301 CAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCA 360  
Db 301 CAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCA 360  
Qy 361 GTCAAAAGCTCTGAACCTATGTTTCAACTATGAGCTACTTGAACCTTGTGGATAGCAAGCT 420  
Db 361 GTCAAAAGCTCTGAACCTATGTTTCAACTATGAGCTACTTGAACCTTGTGGATAGCAAGCT 420  
Qy 421 TGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCACCTGAGGAGAACCT 480  
Db 421 TGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCACCTGAGGAGAACCT 480  
Qy 481 TGAGACTGCCCTCTCCGCTGACTAGAGCCAAAGAGACCGAACTCATGTTTGAAGCTTGTGA 540  
Db 481 TGAGACTGCCCTCTCCGCTGACTAGAGCCAAAGAGACCGAACTCATGTTTGAAGCTTGTGA 540  
Qy 541 GAATCTTAAAGAAAGAGAGAAATGCTGAAAGAGAGAACCAAGCTTTTGGCTAGCCAGAT 600  
Db 541 GAATCTTAAAGAAAGAGAGAAATGCTGAAAGAGAGAACCAAGCTTTTGGCTAGCCAGAT 600  
Qy 601 GGAGAAATATCATCATGTGGGAGCAGAAAGCTGAGATGGAGATGTCACCTGCTGGACAAAT 660

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Db 601 GGAGAAATTAATCATCATGTGGGAGCAGAAAGCTGAGATGGAGATGTCACTGCTGGACAAAT 660
Qy 661 CTCGCAAACTCTCCGGTGAAGTCTCCCACTACTTAATTAATAGCCACCTTAATTAATCGGCGTTG 720
Db 661 CTCGCAAACTCTCCGGTGAAGTCTCCCACTACTTAATTAATAGCCACCTTAATTAATCGGCGTTG 720
Qy 721 AAATCAAAATCCAAAACATATATAATTAATGAAGAAAAAATAAGATATGTAATTAAT 780
Db 721 AAATCAAAATCCAAAACATATATAATTAATGAAGAAAAAATAAGATATGTAATTAAT 780
Qy 781 CCGCTGATAAGGGCGAGCGTTTGTATATCTTAATATCTCTCTTTGGCCAAAGAGACTTTG 840
Db 781 CCGCTGATAAGGGCGAGCGTTTGTATATCTTAATATCTCTCTTTGGCCAAAGAGACTTTG 840
Qy 841 TGTGTGATCTTAAGTAGAGCGGAACTAAGTCAATCTACTCTGTTTAAAGCAAAAGGTTG 900
Db 841 TGTGTGATCTTAAGTAGAGCGGAACTAAGTCAATCTACTCTGTTTAAAGCAAAAGGTTG 900
Qy 901 ATGAACCTTTGACTTATCTGTTGAGAAAAAATAAGAAAAA 943
Db 901 ATGAACCTTTGACTTATCTGTTGAGAAAAAATAAGAAAAA 943
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## RESULT 4

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US-10-225-066A-767
; Sequence 767, Application US/10225066A
; Publication No. US20050160493A9
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: ADAM, Luc J
; APPLICANT: DUBELL, Arnold T
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: PILGRIM, Marsha L
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: REUBER, T. Lynne
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omaira
; APPLICANT: YU, Guo-Liang
; APPLICANT: BROUN, Pierre E
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MB10036-2 US
; CURRENT APPLICATION NUMBER: US/10/225, 066A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/837,444
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 1122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 767
; LENGTH: 943
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-767
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Query Match 100.0%; Score 943; DB 10; Length 943;
Best Local Similarity 100.0%; Pred. No. 2.6e-246;
Matches 943; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGAGAAACGAAAAAATAAGAGAAAAACGCTTAGTATCTCCGGCGACTTTGAAC 60
Db 1 CGAGAAACGAAAAAATAAGAGAAAAACGCTTAGTATCTCCGGCGACTTTGAAC 60
Qy 61 CCAACCTGAGGATCAAAATTAGGGCAAAAGCCCTCTCGAGAGAGAGCCATCGGAAGAAA 120
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Db 61 CCAACCTGAGGATCAAAATTAGGGCAAAAGCCCTCTCGAGAGAGAGCCATCGGAAGAAA 120
Qy 121 ABAACCTAGAAATCAAGCGAATTGAGAAACAAAGTAGCCGACAGTACCTTCTCCAAACG 180
Db 121 ABAACCTAGAAATCAAGCGAATTGAGAAACAAAGTAGCCGACAGTACCTTCTCCAAACG 180
Qy 181 TCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTTCTCTGTGACGATCCGTCGC 240
Db 181 TCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTTCTCTGTGACGATCCGTCGC 240
Qy 241 TCTTCTCGTCTGCTCCGCTCCGCGCAAGCTCTACAGCTTCTCCTCCGCGGATAACCTGGT 300
Db 241 TCTTCTCGTCTGCTCCGCTCCGCGCAAGCTCTACAGCTTCTCCTCCGCGGATAACCTGGT 300
Qy 301 CAAGATCTCTTGATCGATATGGGAAACAGCATGCTGATGATCTTTAAAGCCTTGGATCATCA 360
Db 301 CAAGATCTCTTGATCGATATGGGAAACAGCATGCTGATGATCTTTAAAGCCTTGGATCATCA 360
Qy 361 GTCAAAAGCTCTGAACTATGTTTCAACATATGAGCTACTTGAACCTTGTGATAGCAAGCT 420
Db 361 GTCAAAAGCTCTGAACTATGTTTCAACATATGAGCTACTTGAACCTTGTGATAGCAAGCT 420
Qy 421 TGTGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCAACTGGAGGAACACCT 480
Db 421 TGTGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCAACTGGAGGAACACCT 480
Qy 481 TGAGACTGCCCTCTCCGCTAGAGCCAAAGAACCGAACTCATGTTGAGCTTTGTTGA 540
Db 481 TGAGACTGCCCTCTCCGCTAGAGCCAAAGAACCGAACTCATGTTGAGCTTTGTTGA 540
Qy 541 GAATCTTAAAGAAAAAGGAGAAAAATGCTGAAAGAGAACCCAGGTTTTCGCTAGCCAGAT 600
Db 541 GAATCTTAAAGAAAAAGGAGAAAAATGCTGAAAGAGAACCCAGGTTTTCGCTAGCCAGAT 600
Qy 601 GGAGAAATTAATCATCATGTGGGAGCAGAAAGCTGAGATGGAGATGTCACTGCTGGACAAAT 660
Db 601 GGAGAAATTAATCATCATGTGGGAGCAGAAAGCTGAGATGGAGATGTCACTGCTGGACAAAT 660
Qy 661 CTCGCAAACTCTCCGGTGAAGTCTCCCACTACTTAATTAAGCCACCTTAATAATCGGCGTTG 720
Db 661 CTCGCAAACTCTCCGGTGAAGTCTCCCACTACTTAATTAAGCCACCTTAATAATCGGCGTTG 720
Qy 721 AAATCAAAATCCAAAACATATATAATTAAGAAAAAATAAGATATGTAATTAAT 780
Db 721 AAATCAAAATCCAAAACATATATAATTAAGAAAAAATAAGATATGTAATTAAT 780
Qy 781 CCGCTGATAAGGGCGAGCGTTTGTATATCTTAATATCTCTCTTTGGCCAAAGAGACTTTG 840
Db 781 CCGCTGATAAGGGCGAGCGTTTGTATATCTTAATATCTCTCTTTGGCCAAAGAGACTTTG 840
Qy 841 TGTGTGATCTTAAGTAGAGCGGAACTAAGTCAATCTACTCTGTTTAAAGCAAAAGGTTG 900
Db 841 TGTGTGATCTTAAGTAGAGCGGAACTAAGTCAATCTACTCTGTTTAAAGCAAAAGGTTG 900
Qy 901 ATGAACCTTTGACTTATCTGTTGAGAAAAAATAAGAAAAA 943
Db 901 ATGAACCTTTGACTTATCTGTTGAGAAAAAATAAGAAAAA 943
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## RESULT 5

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US-10-600-948-1
; Sequence 1, Application US/10600948
; Publication No. US20050091717A1
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard
; APPLICANT: Schomburg, Fritz
; APPLICANT: Michaels, Scott
; APPLICANT: Sung, Si-Bum
; TITLE OF INVENTION: Alteration of Flowering Time in Plants
; FILE REFERENCE: 960296.96871
; CURRENT APPLICATION NUMBER: US/10/600,948
; CURRENT FILING DATE: 2003-06-20
```

;; PRIOR APPLICATION NUMBER: US/09/513,775  
;; PRIOR FILING DATE: 2000-02-25  
;; PRIOR APPLICATION NUMBER: 60/121,572  
;; PRIOR FILING DATE: 1999-02-25  
;; PRIOR APPLICATION NUMBER: 60/123,455  
;; PRIOR FILING DATE: 1999-03-05  
;; NUMBER OF SEQ ID NOS: 10  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 1  
;; LENGTH: 797  
;; TYPE: DNA  
;; ORGANISM: Arabidopsis thaliana  
;; FEATURES:  
;; NAME/KEY: CDS  
;; LOCATION: (1)..(588)  
US-10-600-948-1

Query Match 83.2%; Score 784.4; DB 10; Length 797;  
Best Local Similarity 99.9%; Pred. No. 4.8e-203;  
Matches 785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 110 ATGGGAAGAAAAAATAGAAATCAAGCGAATTCAGAAACAAAGTAGCCGACAAAGTCACC 169  
Db 1 ATGGGAAGAAAAAATAGAAATCAAGCGAATTCAGAAACAAAGTAGCCGACAAAGTCACC 60

Qy 170 TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTGTCAGCTTTCTGTCTGTGAC 229  
Db 61 TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTGTCAGCTTTCTGTCTGTGAC 120

Qy 230 GCATCCGTCGCTCTTCGTCGTCCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCGGC 289  
Db 121 GCATCCGTCGCTCTTCGTCGTCCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCGGC 180

Qy 290 GATAACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTTAAAGCC 349  
Db 181 GATAACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTTAAAGCC 240

Qy 350 TTGGATCATCAGTCGCAACGGTCTGAACTATGGTTTCACTATGAGCTACTTGAACCTTTG 409  
Db 241 TTGGATCATCAGTCGCAACGGTCTGAACTATGGTTTCACTATGAGCTACTTGAACCTTTG 300

Qy 410 GATAGCAAGCTTGTGGGATCAAAATGTCAAAAATGTGAGTATCGATGCTCTTGTTCAACTG 469  
Db 301 GATAGCAAGCTTGTGGGATCAAAATGTCAAAAATGTGAGTATCGATGCTCTTGTTCAACTG 360

Qy 470 GAGGAAACCTTTGAGACTGCGCTCTCCGTCGATAGAGCCAAAGACCGAACTCATGTTG 529  
Db 361 GAGGAAACCTTTGAGACTGCGCTCTCCGTCGATAGAGCCAAAGACCGAACTCATGTTG 420

Qy 530 AAGCTTTGTGAGATCTTAAAGAAAGGAGAAATGCTGAAAGAGGAAACCGAGTTTGTG 589  
Db 421 AAGCTTTGTGAGATCTTAAAGAAAGGAGAAATGCTGAAAGAGGAAACCGAGTTTGTG 480

Qy 590 GCTAGCCAGATGAGAAATATCATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACTT 649  
Db 481 GCTAGCCAGATGAGAAATATCATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACTT 600

Qy 650 GCTGGAACAAATCTCCGACAAATCTTCCGTCGACTCTCCCACTACTTAATAGCCACCTTAA 709  
Db 541 GCTGGAACAAATCTCCGACAAATCTTCCGTCGACTCTCCCACTACTTAATAGCCACCTTAA 600

Qy 710 ATCGGCGGTTGAATCAAAATCCAAACATATATATTAATTAAGGAAACCAAAATTAAGAT 769  
Db 601 ATCGGCGGTTGAATCAAAATCCAAACATATATATTAATTAAGGAAACCAAAATTAAGAT 660

Qy 770 ATGTAATTAATTCGCTGATAGGCGGAGCTTTGTATATCTTAATCTCTCTTTGGCC 829  
Db 661 ATGTAATTAATTCGCTGATAGGCGGAGCTTTGTATATCTTAATCTCTCTTTGGCC 720

Qy 830 AAGAGACTTTGTGTGATATCTTAAAGTAGAGGAACTAAAGTCAATATCTATCTGTTTAAAG 889  
Db 721 AAGAGACTTTGTGTGATATCTTAAAGTAGAGGAACTAAAGTCAATATCTATCTGTTTAAAG 780

Qy 890 AAAAA 895  
Db 781 AAAAA 786

RESULT 6  
US-10-905-520-5  
; Sequence 5, Application US/10905520  
; Publication No. US20050160499A1  
; GENERAL INFORMATION:  
; APPLICANT: Richard, AMASINO M.  
; TITLE OF INVENTION: VERNALIZATION-RELATED MOLECULES AND METHODS FOR  
; TITLE OF INVENTION: INDUCIBLY-CONFERRING EPIGENETIC CHANGES  
; FILE REFERENCE: 054030-0076  
; CURRENT APPLICATION NUMBER: US/10/905,520  
; PRIOR FILING DATE: 2005-01-07  
; PRIOR APPLICATION NUMBER: US 60/534,835  
; PRIOR FILING DATE: 2004-01-07  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 591  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-905-520-5

Query Match 62.7%; Score 591; DB 10; Length 591;  
Best Local Similarity 100.0%; Pred. No. 2.5e-150;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 ATGGGAAGAAAAAATAGAAATCAAGCGAATTCAGAAACAAAGTAGCCGACAAAGTCACC 169  
Db 1 ATGGGAAGAAAAAATAGAAATCAAGCGAATTCAGAAACAAAGTAGCCGACAAAGTCACC 60

Qy 170 TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTGTCAGCTTTCTGTCTGTGAC 229  
Db 61 TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTGTCAGCTTTCTGTCTGTGAC 120

Qy 230 GCATCCGTCGCTCTTCGTCGTCCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCGGC 289  
Db 121 GCATCCGTCGCTCTTCGTCGTCCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCGGC 180

Qy 290 GATAACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTTAAAGCC 349  
Db 181 GATAACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTTAAAGCC 240

Qy 350 TTGGATCATCAGTCGCAACGGTCTGAACTATGGTTTCACTATGAGCTACTTGAACCTTTG 409  
Db 241 TTGGATCATCAGTCGCAACGGTCTGAACTATGGTTTCACTATGAGCTACTTGAACCTTTG 300

Qy 410 GATAGCAAGCTTGTGGGATCAAAATGTCAAAAATGTGAGTATCGATGCTCTTGTTCAACTG 469  
Db 301 GATAGCAAGCTTGTGGGATCAAAATGTCAAAAATGTGAGTATCGATGCTCTTGTTCAACTG 360

Qy 470 GAGGAAACCTTTGAGACTGCGCTCTCCGTCGATAGAGCCAAAGACCGAACTCATGTTG 529  
Db 361 GAGGAAACCTTTGAGACTGCGCTCTCCGTCGATAGAGCCAAAGACCGAACTCATGTTG 420

Qy 530 AAGCTTTGTGAGATCTTAAAGAAAGGAGAAATGCTGAAAGAGGAAACCGAGTTTGTG 589  
Db 421 AAGCTTTGTGAGATCTTAAAGAAAGGAGAAATGCTGAAAGAGGAAACCGAGTTTGTG 480

Qy 590 GCTAGCCAGATGAGAAATATCATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACTT 649  
Db 481 GCTAGCCAGATGAGAAATATCATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACTT 600

Qy 650 GCTGGAACAAATCTCCGACAAATCTTCCGTCGACTCTCCCACTACTTAATTAAG 700  
Db 541 GCTGGAACAAATCTCCGACAAATCTTCCGTCGACTCTCCCACTACTTAATTAAG 591

RESULT 7  
US-10-600-948-9

; Sequence 9, Application US/10600948  
; Publication No. US20050091717A1  
; GENERAL INFORMATION:  
; APPLICANT: Amasino, Richard  
; APPLICANT: Schomburg, Fritz  
; APPLICANT: Michaels, Scott  
; APPLICANT: Sung, Si-Bum  
; TITLE OF INVENTION: Alteration of Flowering Time in Plants  
; FILE REFERENCE: 960296.96871  
; CURRENT APPLICATION NUMBER: US/10/600,948  
; CURRENT FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: US/09/513,775  
; PRIOR FILING DATE: 2000-02-25  
; PRIOR APPLICATION NUMBER: 60/121,572  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: 60/123,455  
; PRIOR FILING DATE: 1999-03-05  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 867  
; TYPE: DNA  
; ORGANISM: Brassica rapa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(588)  
US-10-600-948-9

Query Match 47.6%; Score 448.6; DB 10; Length 867;  
Best Local Similarity 84.3%; Pred. No. 2.3e-111;  
Matches 543; Conservative 0; Mismatches 94; Indels 8; Gaps 3;  
  
QY 110 ATGGGAAGAAAAAACTAGAAATCAAGCGAATTGAGAAACAAAGTAGCGGACAAAGTCACC 169  
DB 1 ATGGGAAGAAAAAACTAGAAATCAAGCGAATTGAGAAACAAAGTAGCGGACAAAGTCACC 60  
  
QY 170 TTCTCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTCTGTGTGAC 229  
DB 61 TTCTCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTCTGTGTGAC 120  
  
QY 230 GCATCCGTGCTCTTCTGCTGCTCGGCTCGGCAAGCTCTACAGCTTCTCTCCCGG 289  
DB 121 GCATCTGTGGGCTCTCTGCTGCTCGGCTCGGCAAACTCTACAGCTTCTCTCCCGG 180  
  
QY 290 GATAACCTGGTCAAGATCTTGAATCGATATGGAACACAGCATGCTGATGATCTTAAAGCC 349  
DB 181 GATAGACTGGAGAGATCTTGAATCGATATGGAACAAACATGCTGATGATCTCAATGCC 240  
  
QY 350 TTGGATCATAGTCAAAAGCTCTGAACTATGTTTCACTATGAGCTACTTGAACCTTGTG 409  
DB 241 CTGGATCTTCACTCAAAATCTCTGAACTATAGTTTCAACCATGAGCTACTAGAACTTGTG 300  
  
QY 410 GATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTTGTTCAACTG 469  
DB 301 GAAAGCAAGCTTGTGGAAATCAATTG---ATGATGTAAGCGTGGATTCCTCTCGTGACTA 357  
  
QY 470 GAGGAACACTTTGAGACTCCCTCTCCGTGACTAGAGCCAAAGACCGAACTCATGTGTG 529  
DB 358 GAAGATCACCTTGAGACTGCCCTCTCTGTAATAGAGCTCGGAAGCAGAACTAATGTTA 417  
  
QY 530 AAGCTTTGTGAAGATCTTAAAGAAAGGAGAAATGCTGAAAGAGAGAACAGAGTTTGTG 589  
DB 418 AAGCTTTGTGAAGATCTTAAAGAAAGGAGAAATGCTGAAAGAGAGAACAGAGTTTGTG 477  
  
QY 590 GCTAGCCAGATCGAGATTAATCATCATGTGGGAGCGAAGCTGAGATGAGATGCACT 649  
DB 478 GCTAGTCAATTTGAGAGAAATAATCTTGAGGAGCGGAGAGCTGATAATATAGAGATGCA 537  
  
QY 650 GCTGAGCAAACTCTCCGA---CAATCTTCGGTGTACTCTCCCACTACTTAATTTAGCCACT 706  
DB 538 TCTGGACAATCTCCGACATCAATCTTCTGTAATCTCTCCCGCTGCTTAATTAACCACT 597  
  
QY 707 TAAATCGCGGTTGAAATCAAAATCCAAACATATATATATATGA 751

DB 598 TTACTCGGGGTT--AATCAAAATAAGAAACATATAATCTAAAGA 640  
  
RESULT 8  
US-10-600-948-7  
; Sequence 7, Application US/10600948  
; Publication No. US20050091717A1  
; GENERAL INFORMATION:  
; APPLICANT: Amasino, Richard  
; APPLICANT: Schomburg, Fritz  
; APPLICANT: Michaels, Scott  
; APPLICANT: Sung, Si-Bum  
; TITLE OF INVENTION: Alteration of Flowering Time in Plants  
; FILE REFERENCE: 960296.96871  
; CURRENT APPLICATION NUMBER: US/10/600,948  
; CURRENT FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: US/09/513,775  
; PRIOR FILING DATE: 2000-02-25  
; PRIOR APPLICATION NUMBER: 60/121,572  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: 60/123,455  
; PRIOR FILING DATE: 1999-03-05  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 863  
; TYPE: DNA  
; ORGANISM: Brassica rapa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(588)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (839)  
; OTHER INFORMATION: unsure  
US-10-600-948-7  
  
Query Match 46.6%; Score 439; DB 10; Length 863;  
Best Local Similarity 83.3%; Pred. No. 9.8e-109;  
Matches 537; Conservative 0; Mismatches 100; Indels 8; Gaps 3;  
  
QY 110 ATGGGAAGAAAAAACTAGAAATCAAGCGAATTGAGAAACAAAGTAGCGGACAAAGTCACC 169  
DB 1 ATGGGAAGAAAAAACTAGAAATCAAGCGAATTGAGAAACAAAGTAGCGGACAAAGTCACC 60  
  
QY 170 TTCTCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTCTGTGTGAC 229  
DB 61 TCCTCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTCTGTGTGAC 120  
  
QY 230 GCATCCGTGCTCTTCTGCTGCTCGGCTCGGCAAGCTCTACAGCTTCTCTCCCGG 289  
DB 121 GCATCTGTGGGCTCTCTGCTGCTCGGCTCGGCAAACTCTACAGCTTCTCTCCCGG 180  
  
QY 290 GATAACCTGGTCAAGATCTTGAATCGATATGGAACACAGCATGCTGATGATCTTAAAGCC 349  
DB 181 GATAGACTGGAGAGATCTTGAATCGATATGGAACAAACATGCTGATGATCTCAATGCC 240  
  
QY 350 TTGGATCATAGTCAAAAGCTCTGAACTATGTTTCACTATGAGCTACTTGAACCTTGTG 409  
DB 241 CTGGATCTTCACTCAAAATCTCTGAACTATAGTTTCAACCATGAGCTACTAGAACTTGTG 300  
  
QY 410 GATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTTGTTCAACTG 469  
DB 301 GAAAGCAAGCTTGTGGAAATCAATTG---ATGATGTAAGCGTGGATTCCTCTCGTGACTA 357  
  
QY 470 GAGGAACACTTTGAGACTGCCCTCTCCGTGACTAGAGCCAAAGACCGAACTCATGTGTG 529  
DB 358 GAAGATCACCTTGAGACTGCCCTCTCTGTAATAGAGCTCGGAAGCAGAACTAATGTTA 417  
  
QY 530 AAGCTTTGTGAAGATCTTAAAGAAAGGAGAAATGCTGAAAGAGAGAACAGAGTTTGTG 589  
DB 418 AAGCTTTGTGAAGATCTTAAAGAAAGGAGAAATGCTGAAAGAGAGAACAGAGTTTGTG 477

Qy	590	GCTAGCCAGATGGAGAAATAATCATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACCT	649
Db	478	GCTAGTCAGATTGAGGAGAAAACTCTTGAGGAGCCGAGCTGATAATATAGAGATGTCA	537
Qy	650	GCTGGACAAATCTCCGA---CAATCTCGGTGACTCTCCCACTCTTAATTAATGACCACT	706
Db	538	TCTGGACAAAATCTCCGACATCAATCTTCTGTAACTCTCCCGCTGTTAATTAACCACT	597
Qy	707	TAAATCGGCGGTGGAAATCAAAATCCAAAACATATATAATTATGA	751
Db	598	TTACTCGGCGGTT---AATCAAAATAAGAAAACATATAATCTCAAAGA	640

## RESULT 9

```

US-11-172-740-578
; Sequence 578, Application US/11172740
; Publication No. US20060057724A1
; GENERAL INFORMATION:
; APPLICANT: MASCIA, Peter
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
; TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
; FILE REFERENCE: 2750-1602PUS2
; CURRENT APPLICATION NUMBER: US/11/172,740
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,621
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,800
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 2523
; SEQ ID NO 578
; LENGTH: 884
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(884)
; OTHER INFORMATION: Ceres CLONE ID no. 92459
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(884)
; OTHER INFORMATION: Also known as Ceres CDNA ID no. 23361912
US-11-172-740-578

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Query Match	39.6%	Score 373.6	DB 16	Length 884
Best Local Similarity	73.9%	pred. No. 7.1e-91		
Matches 517	Conservative 0	Mismatches 174	Indels 9	Gaps 3
QY	70	AGGATCAAAATTAGGGGCAAAAGCCCTCTCGAGA---	GAAGCCCATGGGAAGAAAAAACT	126
DB				
	1	AGGATTAAATTAGGGGCA-TAAACCTTTATCGGAGATT	TGAAGCCCATGGGAAGAAAAAAAT	59
QY	127	AGAAATCAAGCGGAATTCGAGAACAAAGTAGCCGACAACT	CACCTTCTCCAAACGTCGCAA	186
DB	60	CGAGATCAAGCGGAATTCGAGAACAAAGTAGCGAAGT	CGAAGTCACTTCTCAACACGACGCA	119
QY	187	CGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTGTT	CGTACGCGATCCGTCGCTCTTCT	246
DB	120	TGGTCTCATCGACAAAGCTCGACAACTTTTCGATT	CTCTGTGAATCTCCGTCGCTGTGT	179
QY	247	CGTTCGCTCCGCTCCGGGAAGCTCTACAGTTCCT	CTCCGGCGGAGATAACCTGGTCAAGAT	306
DB	180	CGTCGTATCTGCCTCCGGAAACTCTATGACTCT	TCTCCTCCGCTGACGCAATTTCCAGAT	239
QY	307	CTTTGATCGATATGGGAAACAGCATGCTGATGAT	CTTTAAAGCCCTTGGATCATCATGTCAAA	366
DB	240	CATTGATCGTTATGAATAACAACATGCTGATGAAC	CTTAGAGCCCTTAGATCTTTGAAGAAAA	299
QY	367	AGCTCTGAACTATGGTTTCACACTATGAGCTACT	TTGAACTCTTGATAGCAAGCTTGTGGG	426

300	AAATTGAGAAATTATCTTCACACAAAGGAGTTACTAGAAACAGCTGCACAAAGCAAGCTTGAAGA	359
427	ATCAAAATGTCAAAAAATGTGAGTATCGATGCTCTTGTTGTTGTTGAGGGAACACCTTGGAGAC	486
360	ACCAAAATGTCGATAATGTAAAGTGTAGAAATCTCTAAATTTCTCTGGAGGGAACAACTTTGAGAC	419
487	TGCGCTCTCCGTTGACTAGAGCCAAAGAGACCGAACTCATGTGTGAAGCTTGTGTGAGAAATCT	546
420	TGCTCTGTCGTAAGTAGAGCTAGGAGGCGAAGAACTGATGATGAGTATATATCGAGTCCCT	479
547	TAAAGAAAAGGAGAGAAAATGCTGAAAGAGAGAAACACAGGTTTTGCTAGCCAGATGGAGAA	606
480	TAAAGAAAAGGAGAGAAAATGTGTGAGAGAGAGAGAACACAGGTTCTGGCTAGCCAGATGGGAAA	539
607	TAAATCATCATGTGGGAGCAGAACTGATGAGATGGAGATGTCACCTGCTGGACAAATCTCCGA	666
540	GAATACGTTGCTGGCAACACATGATGAGAGAGGAATGTTTTCGGGAAGTAGCTCCGGCAA	599
667	CAATCTTTCCGGTGACTCTCCCACTACTTAAATTAGCCACCTTT-----AAATCGGGGTTGA	721
600	CAAAATACCGGAGACTCTCCCGCTGCTCAATTAGCCACCATCATCAACGGCTGAGTTTTC	659
722	AATCAAAATCCAAAAATATATATTAATTATGAGAAAAA	761
660	ACCTTAAACTCAAGCGCTGATTATTAATTAAAGAAATAAA	699

PRCIT.T 10

US-10-225-066A-1087  
; Sequence 1087, Application US/10295066A  
; Publication No. US20030226173A1  
GENERAL INFORMATION:  
; APPLICANT: Mendel Biotechnology, Inc.  
; APPLICANT: RATCLIFFE, Oliver  
; APPLICANT: RIECHMANN, Jose Luis  
; APPLICANT: ADAM, Luc J  
; APPLICANT: DUBELL, Arnold T  
; APPLICANT: HEARD, Jacqueline E  
; APPLICANT: PILGRIM, Marsha L  
; APPLICANT: JIANG, Cai-Zhong  
; APPLICANT: REUBER, T. Lynne  
; APPLICANT: CREELMAN, Robert A  
; APPLICANT: PINEDA, Omalra  
; APPLICANT: YU, Guo-Liang  
; APPLICANT: BROWN, Pierre E  
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants  
; FILE REFERENCE: MBI0036-2 US  
; CURRENT APPLICATION NUMBER: US/10/225,066A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: 09/837,444  
; PRIOR FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: 60/310,847  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 60/336,049  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: 60/338,692  
; PRIOR FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: 10/171,468  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 1122  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1087  
; LENGTH: 883  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-225-066A-1087

Query Match 39.5%; Score 372.6; DB 7; Length 883;  
Best Local Similarity 73.8%; Pred. No. 1.3e-90;  
Matches 489; Conservative 0; Mismatches 169; Indels 5; Gaps 1;  
QY 104 GAAGCCATCGGAGAAAAAACTAGAAATCAAGCGAATTGAGAACAAAACCTAGCCGACAA 163

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Db 25 GAAGCCATGGGAAGAGAAATAATCGAGATCAAGCGAATCGAGAAACAAAGACGTCGACAA 84
Qy 164 GTACACCTTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAAGCTTCTGTCTTC 223
Db 85 GTCACTTCTTCCAAACACGCAATGGTCTCATCGACAAAGCTCGACAACTTTTCAATCTTC 144
Qy 224 TGTGACGCATCCGTCGCTCTTCTCGTCTCCGCTCTCCGCTCCGCAAGCTCTACAGCTTCTCC 283
Db 145 TGTGAATCCCTCCGTCGCTGTGTCTGTATCTGCTTCCGAAACCTCTATGACTCTTCC 204
Qy 284 TCCGGCGATAACTGGTCAAGATCTTGTGATCGATATGGGAAACAGCAATGCTGATGATCTT 343
Db 205 TCCGGTGACGACATTTCCAAAGATCAATGATCGTATGAAATCAACAATGCTGATGAATTT 264
Qy 344 AAAGCCTTGGATCATCATGATCAAGCTCTGAATCTGATGTTTCACTATGAGCTACTTGAA 403
Db 265 AGAGCCTTAGATCTTGAAGAAATAATTCAGAAATTTATCTTCCACACAAAGGATTTACTAGAA 324
Qy 404 CTGTGTGATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTTGTGT 463
Db 325 ACAGTCCAAAGCAAGCTTGAAGAACCAATGTGATATGTAAGTGTAGATTTCTTAAT 384
Qy 464 CAATGTGAGGAAACACCTTGTGAGACTGCGCTCTCCGTGATAGCCCAAGAACCCGAACTC 523
Db 385 TCTCTGAGGAAACAACTTGTGAGACTGCTCTGCTCCGTAAGTATAGGCTAGGAAGGCGAAGTG 444
Qy 524 ATGTTGAGCTTGTGAGAAATCTTAAAGAAAGGAGAAATCTGTAAGAAAGAACCCAG 583
Db 445 ATGATGGAGTATATCGAGTCCCTTAAAGAAAGGAGAAATTCCTCGAGAGAGAACCCAG 504
Qy 584 GTTTTGGCTAGCCAGATGGAGAAATATCATATGTTGGGAGAGAGAGCTGAGATGGAGATG 643
Db 505 GTTCTGGCTAGCCAGATGGAGAAATATCATATGTTGGGAGAGAGAGCTGAGATGGAGATG 564
Qy 644 TCACCTGTGAGCAAAATCTCCGACAACTTCCGCTGACTCTCCCACTACTCTTAATAGCCA 703
Db 565 TTTCCGGGAAGTAGCTCCGCAACAAATAACCGGAGACTCTCCGCTGCTCAATAGCCA 624
Qy 704 CCTT-----AAATCGGCGGTGAAATCAAAATCAAAATCAATATATATATGAGAAAAA 758
Db 625 CCATCATCAACGGCTGAGTTTTTCCCTTAAACTCAAAAGCCTGATTATTAAGAGAAAT 684
Qy 759 AAA 761
Db 685 AAA 687
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## RESULT 11

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US-10-374-780A-15
; Sequence 15, Application US/10374780A
; Publication No. US20040019927A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddle, James
; APPLICANT: Brown, Pierre E
; APPLICANT: Filgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
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; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 883
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G157
US-10-374-780A-15

Query Match 39.5%; Score 372.6; DB 8; Length 883;
Best Local Similarity 73.8%; Pred. No. 1.3e-90;
Matches 489; Conservative 0; Mismatches 169; Indels 5; Gaps 1;

Qy 104 GAAGCCATGGGAAGAAATAATCGAGATCAAGCGAATTCAGAAACAAAGTATCGACAA 163
Db 25 GAAGCCATGGGAAGAAATAATCGAGATCAAGCGAATTCAGAAACAAAGTATCGACAA 84
Qy 164 GTACACCTTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAAGCTTCTGTCTTC 223
Db 85 GTCACTTCTTCCAAACACGCAATGGTCTCATCGACAAAGCTCGACAACTTTTCAATCTTC 144
Qy 224 TGTGACGCATCCGTCGCTCTTCTCGTCTCCGCTCTCCGCAAGCTCTACAGCTTCTTC 283
Db 145 TGTGAATCCCTCCGCTGCTGTGTCTGCTGATCTGCTCCGAAACCTCTATGACTCTTCC 204
Qy 284 TCCGGCGATAACTGGTCAAGATCTTGTGATCGATATGGGAAACAGCAATGCTGATGATCTT 343
Db 205 TCCGGTGACGACATTTCCAAAGATCAATGATCGTATGAAATCAACAATGCTGATGAATTT 264
Qy 344 AAAGCCTTGGATCATCATGATCAAGCTCTGAAACTATGTTTCACTATGAGCTACTTGAA 403
Db 265 AGAGCCTTAGATCTTGAAGAAATAATTCAGAAATTTATCTTCCACACAAAGGATTTACTAGAA 324
Qy 404 CTTTGGATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTTGTGT 463
Db 325 ACAGTCCAAAGCAAGCTTGAAGAACCAATGTGATATGTAAGTGTAGATTTCTTAAT 384
Qy 464 CAACTGGAGGAAACCTTGTGAGACTGCGCTCTCCGCTGACTAGAGCCCAAGAACCCGAACTC 523
Db 385 TCTCTGGAGGAAACAACTTGTGAGACTGCTCTGCTCCGTAAGTATAGGCTAGGAAGGCGAAGTG 444
Qy 524 ATGTTGAAAGCTTGTGAGAAATCTTAAAGAAAGGAGAAATCTGTAAGAAAGAACCCAG 583
Db 445 ATGATGGAGTATATCGAGTCCCTTAAAGAAAGGAGAAATTCCTCGAGAGAGAACCCAG 504
Qy 584 GTTTTGGCTAGCCAGATGGAGAAATATCATATGTTGGGAGAGAGAGCTGAGATGGAGATG 643
Db 505 GTTCTGGCTAGCCAGATGGAGAAATATCATATGTTGGGAGAGAGAGCTGAGATGGAGATG 564
Qy 644 TCACCTGTGAGCAAAATCTCCGACAACTTCCGCTGACTCTCCCACTACTCTTAATAGCCA 703
Db 565 TTTCCGGGAAGTAGCTCCGCAACAAATAACCGGAGACTCTCCGCTGCTCAATAGCCA 624
Qy 704 CCTT-----AAATCGGCGGTGAAATCAAAATCAAAATCAATATATATATGAGAAAAA 758
Db 625 CCATCATCAACGGCTGAGTTTTTCCCTTAAACTCAAAAGCCTGATTATTAAGAGAAAT 684
Qy 759 AAA 761
Db 685 AAA 687
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Db 625 CCATCATCAACGGCTGAGTTTTCACCTTAAACTCAAGCCTGATTTCATAATTAAGAGAT 684

Qy 759 AAA 761

Db 685 AAA 687

## RESULT 12

US-10-412-699B-69

; Sequence 69, Application US/10412699B

; Publication No. US20040045049A1

; GENERAL INFORMATION:

; APPLICANT: Mendel Biotechnology, Inc.

; APPLICANT: Zhang, James

; APPLICANT: Fromm, Michael E.

; APPLICANT: Heard, Jacqueline E.

; APPLICANT: Riechmann, Jose Luis

; APPLICANT: Adam, Luc J.

; APPLICANT: Broun, Pierre E.

; APPLICANT: Pineda, Omaisra

; APPLICANT: Reuber, T. Lynne

; APPLICANT: Keddle, James S.

; APPLICANT: Yu, Guo-Liang

; APPLICANT: Jiang, Cai-Zhong

; APPLICANT: Samaha, Raymond R.

; APPLICANT: Pilgrim, Marsha L.

; APPLICANT: Creelman, Robert A.

; APPLICANT: DuBell, Arnold N.

; APPLICANT: Ratcliffe, Oliver

; APPLICANT: Kumimoto, Roderick

; APPLICANT: Sherman, Bradley K.

; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants

; FILE REFERENCE: MBI-0048CIP

; CURRENT APPLICATION NUMBER: US/10/412.699B

; CURRENT FILING DATE: 2003-04-10

; PRIOR APPLICATION NUMBER: 09/394,519

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: 09/489,376

; PRIOR FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: 09/506,720

; PRIOR FILING DATE: 2000-02-17

; PRIOR APPLICATION NUMBER: 09/533,030

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/533,392

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/533,029

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/532,591

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/533,648

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/713,994

; PRIOR FILING DATE: 2000-11-16

; PRIOR APPLICATION NUMBER: 09/819,142

; PRIOR FILING DATE: 2001-03-27

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 2011

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 69

; LENGTH: 883

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; OTHER INFORMATION: G157

US-10-412-699B-69

Query Match 39.58; Score 372.6; DB 8; Length 883;

Best Local Similarity 73.8; Pred. No. 1.3e-90;

Matches 489; Conservative 0; Mismatches 169; Indels 5; Gaps 1;

Qy 104 GAAGCCATGGAGAAAAAATAGAAATCAAGCGAATTCAGAACCAAAAGTAGCCGACAA 163

Db 25 GAAGCCATGGAGAAAAAATAGAAATCAAGCGAATTCAGAACCAAAAGTAGCCGACAA 84

Qy 164 GTACACCTTCTCCAAACGCTCGCAACGGTCTCATATCAGAAAAAGCTCGTCAAGCTTCTGTTCTC 223

Db 85 GTACACCTTCTCCAAACGCTCGCAACGGTCTCATATCAGAAAAAGCTCGTCAAGCTTCTGTTCTC 144

Qy 224 TGTGACGCATCCGTCGCTCTTCTGCTGCTCTCCGCTCGGCAAGCTCTACAGCTTCTCC 283

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Qy 284 TCCGGCGATAAACCTGGTCAAGATCCTTGTATGCGATATGGGAAACAGCATGCTGATGATCTT 343

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Qy 344 AAAGCCTTGGATCATCATAGTCAAAAGCTCTGAACTATGTTTCACTATGAGCTACTTGAA 403

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Qy 404 CTTGTGGATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGT 463

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Qy 759 AAA 761

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## RESULT 13

US-10-412-699B-1733

; Sequence 1733, Application US/10412699B

; Publication No. US20040045049A1

; GENERAL INFORMATION:

; APPLICANT: Mendel Biotechnology, Inc.

; APPLICANT: Zhang, James

; APPLICANT: Fromm, Michael E.

; APPLICANT: Heard, Jacqueline E.

; APPLICANT: Riechmann, Jose Luis

; APPLICANT: Adam, Luc J.

; APPLICANT: Broun, Pierre E.

; APPLICANT: Pineda, Omaisra

; APPLICANT: Reuber, T. Lynne

; APPLICANT: Keddle, James S.

; APPLICANT: Yu, Guo-Liang

; APPLICANT: Jiang, Cai-Zhong

; APPLICANT: Samaha, Raymond R.

; APPLICANT: Pilgrim, Marsha L.

; APPLICANT: Creelman, Robert A.

; APPLICANT: DuBell, Arnold N.

; APPLICANT: Ratcliffe, Oliver

; APPLICANT: Kumimoto, Roderick

; APPLICANT: Sherman, Bradley K.

; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants

; FILE REFERENCE: MBI-0048CIP

; CURRENT APPLICATION NUMBER: US/10/412.699B

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/ CURRENT FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: 09/394,519
/ PRIOR FILING DATE: 1999-09-13
/ PRIOR APPLICATION NUMBER: 09/489,376
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: 09/506,720
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: 09/533,030
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/533,392
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/533,029
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/532,591
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/533,648
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/713,994
/ PRIOR FILING DATE: 2000-11-16
/ PRIOR APPLICATION NUMBER: 09/819,142
/ PRIOR FILING DATE: 2001-03-27
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2011
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1733
/ LENGTH: 883
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-10-412-699B-1733

Query Match      39.5%; Score 372.6; DB 8; Length 883;
Best Local Similarity 73.8%; Pred. No. 1.3e-90;
Matches 489; Conservative 0; Mismatches 169; Indels 5; Gaps 1;

QY 104 GAAGCCATGGGAGAAAAAAGCTAGAAATCAAGCGAATTGAGAACAAAAGTAGCCGACAA 163
Db 25 GAAGCCATGGGAGAAAAAAGCTAGAAATCAAGCGAATTGAGAACAAAAGTAGCCGACAA 84

QY 164 GTCACTTCTCCAAAGCTGCGAAGCTGTCATCGAAGAGCTGTCAGCTTTCTGTCTC 223
Db 85 GTCACTTCTCCAAAGCTGCGAAGCTGTCATCGAAGAGCTGTCAGCTTTCTGTCTC 144

QY 224 TGTGAGCGATCGTGGTCTTCTCGTCTCTCCGCTCGGCAAGCTCTACAGCTTCTCC 283
Db 145 TGTGAATCCTCGTGGCTGTTGTGTCGTCTCGGCAAGCTCTATGACTTCTCC 204

QY 284 TCCGCGGATAACCTCGGTCAAGATCCTTGATCGAATGGAACACGATGCTGATGATCTT 343
Db 205 TCCGCTGACGACATTTCCAAAGATCATTCGTTATGAATACACATGCTGATGACTT 264

QY 344 AAAGCCTTGGATCATCACTGCAAGCTCTGAAAGCTCTGAAAGCTCTGAAAGCTCTGAA 403
Db 265 AAAGCCTTGGATCATCACTGCAAGCTCTGAAAGCTCTGAAAGCTCTGAAAGCTCTGAA 624

/ CURRENT FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: 09/394,519
/ PRIOR FILING DATE: 1999-09-13
/ PRIOR APPLICATION NUMBER: 09/489,376
/ PRIOR FILING DATE: 2000-01-21
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/ PRIOR APPLICATION NUMBER: 09/533,648
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/713,994
/ PRIOR FILING DATE: 2000-11-16
/ PRIOR APPLICATION NUMBER: 09/819,142
/ PRIOR FILING DATE: 2001-03-27
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2011
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1733
/ LENGTH: 883
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-10-412-699B-1733

Query Match      39.5%; Score 372.6; DB 8; Length 883;
Best Local Similarity 73.8%; Pred. No. 1.3e-90;
Matches 489; Conservative 0; Mismatches 169; Indels 5; Gaps 1;

QY 104 GAAGCCATGGGAGAAAAAAGCTAGAAATCAAGCGAATTGAGAACAAAAGTAGCCGACAA 163
Db 25 GAAGCCATGGGAGAAAAAAGCTAGAAATCAAGCGAATTGAGAACAAAAGTAGCCGACAA 84

QY 164 GTCACTTCTCCAAAGCTGCGAAGCTGTCATCGAAGAGCTGTCAGCTTTCTGTCTC 223
Db 85 GTCACTTCTCCAAAGCTGCGAAGCTGTCATCGAAGAGCTGTCAGCTTTCTGTCTC 144

QY 224 TGTGAGCGATCGTGGTCTTCTCGTCTCTCCGCTCGGCAAGCTCTACAGCTTCTCC 283
Db 145 TGTGAATCCTCGTGGCTGTTGTGTCGTCTCGGCAAGCTCTATGACTTCTCC 204

QY 284 TCCGCGGATAACCTCGGTCAAGATCCTTGATCGAATGGAACACGATGCTGATGATCTT 343
Db 205 TCCGCTGACGACATTTCCAAAGATCATTCGTTATGAATACACATGCTGATGACTT 264

QY 344 AAAGCCTTGGATCATCACTGCAAGCTCTGAAAGCTCTGAAAGCTCTGAAAGCTCTGAA 403
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/ CURRENT FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: 09/394,519
/ PRIOR FILING DATE: 1999-09-13
/ PRIOR APPLICATION NUMBER: 09/489,376
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: 09/506,720
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: 09/533,030
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/533,392
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/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/713,994
/ PRIOR FILING DATE: 2000-11-16
/ PRIOR APPLICATION NUMBER: 09/819,142
/ PRIOR FILING DATE: 2001-03-27
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2011
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1733
/ LENGTH: 883
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-10-412-699B-1733

Query Match      39.5%; Score 372.6; DB 10; Length 883;
Best Local Similarity 73.8%; Pred. No. 1.3e-90;
Matches 489; Conservative 0; Mismatches 169; Indels 5; Gaps 1;

QY 104 GAAGCCATGGGAGAAAAAAGCTAGAAATCAAGCGAATTGAGAACAAAAGTAGCCGACAA 163
Db 25 GAAGCCATGGGAGAAAAAAGCTAGAAATCAAGCGAATTGAGAACAAAAGTAGCCGACAA 84

QY 164 GTCACTTCTCCAAAGCTGCGAAGCTGTCATCGAAGAGCTGTCAGCTTTCTGTCTC 223
Db 85 GTCACTTCTCCAAAGCTGCGAAGCTGTCATCGAAGAGCTGTCAGCTTTCTGTCTC 144

QY 224 TGTGAGCGATCGTGGTCTTCTCGTCTCTCCGCTCGGCAAGCTCTACAGCTTCTCC 283
Db 145 TGTGAATCCTCGTGGCTGTTGTGTCGTCTCGGCAAGCTCTATGACTTCTCC 204

QY 284 TCCGCGGATAACCTCGGTCAAGATCCTTGATCGAATGGAACACGATGCTGATGATCTT 343
Db 205 TCCGCTGACGACATTTCCAAAGATCATTCGTTATGAATACACATGCTGATGACTT 264

QY 344 AAAGCCTTGGATCATCACTGCAAGCTCTGAAAGCTCTGAAAGCTCTGAAAGCTCTGAA 403
Db 265 AAAGCCTTGGATCATCACTGCAAGCTCTGAAAGCTCTGAAAGCTCTGAAAGCTCTGAA 624
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## RESULT 15

US-10-225-066A-1055  
; Sequence 1055, Application US/10225066A  
; Publication No. US20030226173A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendel Biotechnology, Inc.  
; APPLICANT: RATCLIFFE, Oliver  
; APPLICANT: RIECHMANN, Jose Luis  
; APPLICANT: ADAM, Luc J  
; APPLICANT: DUBELL, Arnold T  
; APPLICANT: HEARD, Jacqueline E  
; APPLICANT: PILGRIM, Mareha L  
; APPLICANT: JIANG, Cai-Zhong  
; APPLICANT: REUBER, T. Lynne  
; APPLICANT: CREELMAN, Robert A  
; APPLICANT: PINEDA, Omeira  
; APPLICANT: YU, Guo-Liang  
; APPLICANT: BROUN, Pierre E  
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants  
; FILE REFERENCE: MB10036-2 US  
; CURRENT APPLICATION NUMBER: US/10/225,066A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: 09/837,444  
; PRIOR FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: 60/310,847  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 60/336,049  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: 60/338,692  
; PRIOR FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: 10/171,468  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 1122  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1055  
; LENGTH: 1059  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-225-066A-1055

Query Match 38.6%; Score 363.8; DB 7; Length 1059;  
Best Local Similarity 73.9%; Pred. No. 3.7e-88;  
Matches 475; Conservative 0; Mismatches 167; Indels 1; Gaps 1;

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QY 247 CGTGTCTCCGCTCCCGCAAGCTCTACAGCTTCTCTCCGCGGATAACCTGGTCAAGAT 306  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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## SUMMARIES

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3	63.8	6.8	846	7 US-11-217-529-1966	Sequence 1966, Ap
4	56	5.9	1968	7 US-11-217-529-2608	Sequence 2608, Ap
5	54.8	5.8	4077	6 US-10-505-928-134	Sequence 134, App
6	54.4	5.8	534	7 US-11-217-529-77959	Sequence 77959, A
7	49.6	5.3	804	7 US-11-217-529-82725	Sequence 82725, A
8	46.4	4.9	1362	7 US-11-217-529-82782	Sequence 7782, Ap
9	44.8	4.8	1359	7 US-11-217-529-75588	Sequence 75588, A
10	37.2	3.9	1503	7 US-11-217-529-1697	Sequence 1697, Ap
11	33.6	3.6	475	6 US-10-488-619-1723	Sequence 1723, Ap
12	33.6	3.6	4464	7 US-11-217-529-76543	Sequence 76543, A
13	33.4	3.5	2700	7 US-11-217-529-77867	Sequence 77867, A
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15	33	3.5	641	6 US-10-488-619-1577	Sequence 1577, Ap
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17	32.8	3.5	1556	6 US-10-505-928-322	Sequence 322, App
18	32.6	3.5	918	7 US-11-217-529-1084	Sequence 1084, Ap
19	32.4	3.4	1551	7 US-11-217-529-79695	Sequence 79695, A
20	31.8	3.4	592	6 US-10-488-619-1012	Sequence 1012, Ap
21	31.6	3.4	2025	6 US-10-511-937-414	Sequence 414, App
22	31.6	3.4	394191	6 US-10-506-549-3	Sequence 3, Appli
23	31.4	3.3	228	7 US-11-217-529-166541	Sequence 166541, A
24	31.4	3.3	677	6 US-10-488-619-1302	Sequence 1302, Ap
25	31.4	3.3	855	7 US-11-217-529-5202	Sequence 5202, Ap

## ALIGNMENTS

## RESULT 1

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US-11-217-529-4894
; Sequence 4894, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4894
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4894

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## RESULT 2

RESUL 2  
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; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED



## US-10-505-928-134

Query Match 5.8%; Score 54.8; DB 6; Length 4077;  
Best Local Similarity 55.9%; Pred. No. 9.5e-06;  
Matches 104; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

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Db |||||  
Qy 400 CTATGGGAGAAAAAAGATTGAGATTACGAGATTATGGATGACGTAACGACAGAGGTGA 459  
Db |||||  
Qy 168 CTTTCTCAAAAGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTCTCTGTG 227  
Db |||||  
Qy 460 CATTTACAAAGAGAAATTTGGTTGATGAAGAGGCTTATGAGCTGAGCGTGTGTGTG 519  
Db |||||  
Qy 228 AGCATCGCTCGCTCTTCTGCTCGCTCGCTCGCGCAAGCTCTACAGCTTCTCTCCG 287  
Db |||||  
Qy 520 ACTGTGAGATTGCGCTGATCATCTTCAACAGCACCAACAGCTGTTCCAGTATGCCAGCA 579  
Db |||||  
Qy 288 GCGATA 293  
Db 580 CCGACA 585

## RESULT 6

US-11-217-529-77959  
; Sequence 77959, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 77959  
; LENGTH: 534  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-77959

Query Match 5.8%; Score 54.4; DB 7; Length 534;  
Best Local Similarity 59.9%; Pred. No. 4.3e-06;  
Matches 91; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 131 ATCAAGCGAATTGAGAACAAAAGTAGCCGACAAAGTCAACCTTCTCCAAACGTCGCAACGGT 190  
Db |||||  
Qy 253 ATCAGGTACATCGAGATAAGACCCGAGACATGTCACCTTCTCGAAGAGCGGCACGGG 312  
Db |||||  
Qy 191 CTCAATCGAGAAAGCTCGTCAGCTTTCTGTGTCAGCATCCGTCGCTCTTCTCTCGTC 250  
Db |||||  
Qy 313 ATCATGAAAAAGCATATGAGCTCTCCGTCCTACCGGGCCATATCTGCTCTTAATT 372  
Db |||||  
Qy 251 GTCTCCGCTCCGCAAGCTCTACAGCTTCTC 282  
Db 373 CTGGCAAACTCTGGCCTGGTCTACACTTTTCA 404

## RESULT 7

US-11-217-529-82725  
; Sequence 82725, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA

; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 82725  
; LENGTH: 804  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-82725

Query Match 5.3%; Score 49.6; DB 7; Length 804;  
Best Local Similarity 54.3%; Pred. No. 0.0001;  
Matches 100; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 110 ATGGGAGAAAAAATCTAGAAATCAAGCGAATTGAGAACAAAAGTAGCCGACAAAGTCA 169  
Db 1 ATGGGTAGACGGAAGATTGAAATCCAGAGGATTTCTGATGACAGAAATAGGGCTGTCA 60  
Qy 170 TTCTCCAAAAGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTCTGTGAC 229  
Db |||||  
Qy 61 TTTATAAAGCTAAAGCTGGCCCTTTTAAAGAGGCCCATGAACATATCCGTTCTTTGTCAA 120  
Qy 230 GCATCCGTCGCTCTTCTCGCTCGCTCCGCTCCGCGAAGCTCTACAGCTTCTCTCCGGC 289  
Db 121 GTAGACATAGCCGTCATTATATCTGGGGTCCAATAACACGTTCTATGAGTTTCTCTGTG 180  
Qy 290 GATA 293  
Db 181 GATA 184

## RESULT 8

US-11-217-529-2782  
; Sequence 2782, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2782  
; LENGTH: 1362  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-2782

Query Match 4.9%; Score 46.4; DB 7; Length 1362;  
Best Local Similarity 53.3%; Pred. No. 0.001;  
Matches 98; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 110 ATGGGAGAAAAAATCTAGAAATCAAGCGAATTGAGAACAAAAGTAGCCGACAAAGTCA 169  
Db 1 ATGGGTAGAGAAAGATTGAGATTGAGCTTATCAAGGACGATAGAAATCGTACGTA 60  
Qy 170 TTCTCCAAAAGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTCTGTGAC 229  
Db |||||

Db 61 TTCTATAAAGCAAGAGGACTTTTCAGAAAAGCTCATGAAGCTGTCCGACTATGCGCAA 120  
Qy 230 GCATCCGCTGCTTCTCGTGTCTCGGCTCCGCAAGCTCTACAGCTTCTCTCCGGC 289  
Db 121 GTGATATTGCTGTCAATTATATTGGATCATTAATAATACCTTTATGAATACTCTTCTGTC 180  
Qy 290 GATA 293  
Db 181 GATA 184

RESULT 9  
US-11-217-529-75588  
; Sequence 75588, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; PRIOR FILING DATE: 2005-09-02  
; PRIOR FILING DATE: 2005-09-02  
; PRIOR FILING DATE: 2005-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 75588  
; LENGTH: 1359  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-75588

Query Match 4.8%; Score 44.8; DB 7; Length 1359;  
Best Local Similarity 52.7%; Pred. No. 0.0027;  
Matches 97; Conservative 0; Mismatches 87; Indels 0; Gaps 0;  
Qy 110 ATGGGAGAAAAAATAGAAATCAAGCGAATTGAGAACAAAAGTAGCCGACAAAGTCACC 169  
Db 1 ATGGGTAGAGAAAAATTGAATTTGAACCTATCAAGATGATAGAAATCGTACAGTTACT 60  
Qy 170 TTCTCAAAAGCTGCCAAGCTCTCATCGAGAAAGCTCTCAGCTTCTCTCTCTGTGAC 229  
Db 61 TTCTAAAGCAAGAGAGACTGTTTAAAGGCTCATGAATGTGACGACTTTTCCCAA 120  
Qy 230 GCATCCGCTGCTTCTCGTGTCTCGGCTCCGCAAGCTCTACAGCTTCTCTCCGGC 289  
Db 121 GTAGACATTGCTGTCAATTATTTAGGATCCAATAATACATTCTACGAATACCTCTCTGTT 180  
Qy 290 GATA 293  
Db 181 GATA 184

RESULT 10  
US-11-217-529-1697  
; Sequence 1697, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182

; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1697  
; LENGTH: 1503  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-1697

Query Match 3.9%; Score 37.2; DB 7; Length 1503;  
Best Local Similarity 50.6%; Pred. No. 0.32;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
Qy 458 CTTGTTCAACTGGAGGAAACACCTTGAGACTGCGCTCTCCGTGACTAGAGCCAAAGAGACC 517  
Db 922 CTTATTGGCTTGAAGAATAGGTTACATGGACTTTGATGAACAACGCAAAAAGACG 981  
Qy 518 GAACTCATGTTGAAGCTTTGTTGAGAAATCTTAAAGAAAAGGAGAAAATGCTGAAAGAGAG 577  
Db 982 ACGCAAGAGGAGAGAACTGGATGCGAATGAAGATGACAAAAATATTGAACACAGAAACATGAC 1041  
Qy 578 AACCAGTTTTGGCTAGCCAGATGGAGAAATATCATCATGTGGGAGCAGAGCTGAGA 635  
Db 1042 CATGAGGTTTGTGATGCGCAAGATTGATGGTACCGAAAAGTGTTCATGACATGATGATA 1099

RESULT 11  
US-10-488-619-1723/c  
; Sequence 1723, Application US/10488619  
; Publication No. US20060099578A1  
; GENERAL INFORMATION:  
; APPLICANT: Greenlee, Winner and Sullivan, P. C.  
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations  
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays  
; FILE REFERENCE: 98-01 WO  
; CURRENT APPLICATION NUMBER: US/10/488,619  
; CURRENT FILING DATE: 2004-03-01  
; NUMBER OF SEQ ID NOS: 3040  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1723  
; LENGTH: 475  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-488-619-1723

Query Match 3.6%; Score 33.6; DB 6; Length 475;  
Best Local Similarity 51.3%; Pred. No. 1.6;  
Matches 78; Conservative 0; Mismatches 74; Indels 0; Gaps 0;  
Qy 490 CCTCTCCGTGACTAGAGCCCAAGAGACCGAATCATGTTGAAGCTTGTGAGAACTTAA 549  
Db 163 CTTCTCCGAGCTGGCTGAGGACAAAGAAACGGGAGAGGAGATCAGTGTATGAGGC 104  
Qy 550 AGAAAAGGAGAAAATGCTGAAAAGAGAGAAACAGAGTTTGGCTAGCCAGATGGAGATAA 609  
Db 103 AGAGGAGAGAAAGGCTGAGAAAGAGAGGAGAAATAGGAGGATGAGGAGAGCCTAAGAT 44  
Qy 610 TCATCATGTGGAGCAGAGCTGAGATGGAGA 641  
Db 43 TGAAGATGGGATCCGATGAGGAAGATGACA 12

RESULT 12  
US-11-217-529-76543  
; Sequence 76543, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO



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; LENGTH: 641
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1577

Query Match      3.5%; Score 33; DB 6; Length 641;
Best Local Similarity 50.3%; Pred. No. 2.8;
Matches 81; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 3 AGAARAGGAAAAAATAGAAAGAGAAAGCGCTTAGTATCTCGGCGACTTGNACCC 52
Db 357 AACAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 416
QY 63 AAACCTGAGGATCAAAATTAGGGCACAAGCCCTCTCGGAGAGAGCCATGGGAAGAAAA 122
Db 417 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 476
QY 123 AACTAGAAATCAAGCGAATTGAGAACAAAAAGTAGCCGACAA 163
Db 477 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 517
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